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G49140 SHGC-79840
AC154950 Bos tauru
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2 CS206711
2 AR716222
3 BD078048
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4 AR716223
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6 AB096077
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7 AB096079
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CS206709 Sequence
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AR454561 Sequence
BC02249 Homo sapi
BC035057 Homo sapi
AX888567 Synthetic
AX891216 Synthetic
AX891216 Synthetic
BT019710 Sequence
AX377859 Sequence
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AX709626 Sequence
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AC134649 Mus muscu
BV654723 S216P6201
DQ066599 Homo sapi
AC092290 Homo sapi
AC092290 Homo sapi
AC104115 Homo sapi
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AC113172 Rattus no
AC123181 Rattus no
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AC123181 Rattus no
AC136706 Medicago
AC147484 Medicago
AC166237 Medicago
AC16237 AC16237 Medicago
AC16237 AC16

Sequence

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94
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Gaps between the contigs are represented as 100 N.
* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                             69466
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Homo sapiens chromosome 4 clone 2242B18 map 4q22-q24, ***
SEQUENCING IN PROGRESS ***, 3 unordered pieces.
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AP001967.1 GI:7678857
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 120407)
ATGCACAATTGTGTATTAGATTCTGTGGCTAGCAAACGAAAAATTTTTCCAAGCTGACCTT
                                           AATAAGTAAATTGTCTCAAGTCATACTAAAGCACATTACTAGGATCAGTAAAAAATATAT
                                                           ACATTTTCTAAAACTCTTTATAGTGAGAGCATAGGTCTTAGGAAAAATATATTAGCATT
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136240
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                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
                                                                                                                                                                                                                           /clone="2242B18"
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                                                                                                                                                                                                                                                                                                                                     87654: contig of 87654 bp in length
87754: gap of 100 bp
107685: contig of 19931 bp in length
107785: gap of 100 bp
120407: contig of 12622 bp in length
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                                                                                                                              Maillinea...,
Hominidae; Homo.
1 (bases 1 to 165223)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Toward Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                           165223 bp
Homo sapiens BAC clone RP13-514E23
AC104059
AC104059.5 GI:18677547
    Direct Submission
Submitted (03-DEC-2001) Genome
University School of Medicine,
                                                                    2 (bases 1 to 165223)
Wang,C. and Cotton,M.
The sequence of Homo sapiens
Unpublished (2001)
                                              3 (bases 1 to 165223) Waterston, R.H.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                        Bource
                                                                                                                                                                                                                                                                                                     Penale blood was obtained via a double-blind selection protocol. Female blood DNA was isolated from one randomly chosen donor (out of 10 female donors) and partially digested with a combination of ECORI and ECORI whethylase for library segments 1k2 or either MboI or DpnII for library segments 3k4. Size selected DNA was cloned into the pBACe3.6 vector between the ECORI sites for library segments 1k2 or the BamHI sites for library segments 3k4. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). The library has been arrayed into 384-well microtiter dishes and also gridded onto 22x22cm nylon high density filters for screening by probe hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MO 63108, USA 4 (bases 1 to Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
The RPCI-13 Human Female BAC Library was constructed using improved cloning techniques developed by Kazutoyo Osoegawa. The library was generated by Baohui Zhao in our laboratory. Construction was funded by a grant from the National Human Genome Research Institute (NHGRI, NIH) (#1R01RG01165-03). The library was generated according to the new NHGRI/DOE 'Guidance on Human Subjects in Large-Scale DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality sequences); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
5 (bases 1 to 165223)
Waterston,R.
                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restriction
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                                                                                                                                                                                              clone sequenced to the left is RP11-375K17.
s clone is at base position 1 of RP13-514E23;
e position 165223 of RP13-514E23.
                                                                                                                        from AC012208 was used to finish AC104059. Polymorphisms exist een AC012208 and AC104059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: H_FH0514E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu/gsc
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                                                                                                    Location/Qualifiers
  organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/note="similar to
(NID:g17088280)"
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vw02e03.r1"
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/note="similar to Mus musculus EST BI697031
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2759. .3201
                                                                      note="match to EST BG576372 (NID:g13584025)"
                                                                                                                                                                     note="match to
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/note="similar to Homo sapiens EST H19314 (NID:g885554)
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1353. .4368
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1916. .2228
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/rpt_family="L2"
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(NID:g15345757)"
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1528. .1686
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203. .3345
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774. .1819
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CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCCAAGAAATTACACAAGTACTAG
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                                                          ATAAAACTAAAATCATTATAAGGACACAACCATGTGATATTTGTCCATCTGCTCTTTAAG
                                                                                ATAAAACTAAAATCATTATAAGGACACAACCATGTGATATTTGTCCATCTGCTCTTTAAG
                                                                                                                             TGTACTGGATCATTACCATCAGAATAATCAGAATGAATGCCACACTGAATATCAAAAGAA
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5292. .5586
/note="similar to Mus musculus EST BB321301
(NID:g9029615)"
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/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match to EST BF854904 (NID:g12242648),"
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/note="match to EST N28367 (NID:gl146603) yx26f08.
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. .6967
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Pred. No. 1.
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. 1.5e-235;
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AC012208/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CE 2 (bases 1 to 175425)

RRS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barra, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Forreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J., Howland, C.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lieboczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, D., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McEwan, J., Norman, C.H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stanger-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33500
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On May 26, 2000 this sequence version replaced gi:6454052. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175425 bp
Homo sapiens chromosome 4 clone
SEQUENCE, 12 unordered pieces.
AC012208
                                                                                                                                                                                                                                                                                                                                                           AC012208.3 GI:8096853
HTG; HTGS_PHASE1; HTGS_DRAFT
Homo sapiens (human)
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Mammalia; Eutheria; Euarchontoglires; Primates; Cata
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Center project name: L1753

Center clone name: 375 K 17

Center clone name: 375 K 17

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.96731

Consensus quality: 114873 bases at least Q40

Consensus quality: 1161974 bases at least Q30

Consensus quality: 170540 bases at least Q20
                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                          Center code: WIBR web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nusbaum,C.
me 4, clone
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Insert size: 174325; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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                   /note="assembly_fragment"
44214. .44313
                                                  /estimated
32602. .447
                                                                                                                    /estimated_length=100
22118. .32501
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22018. .22117
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14863. .14962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                             note="assembly_fragment"
                                                                                                                                                                                      estimated_length=100
14963. .22017
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1 14862: contig of 8242 bp in length
3 14962: gap of 100 bp
3 22017: contig of 7055 bp in length
8 22117: gap of 100 bp
32501: contig of 10384 bp in length
9 32501: contig of 10384 bp in length
2 32601: gap of 100 bp
32601: gap of 100 bp
44213: contig of 11612 bp in length
4313: gap of 100 bp
57141: contig of 12828 bp in length
57241: gap of 100 bp
57141: contig of 12828 bp in length
71807: gap of 100 bp
87718: contig of 14466 bp in length
187718: contig of 15911 bp in length
187818: gap of 100 bp
120478: contig of 3260 bp in length
120578: gap of 100 bp
175425: contig of 54847 bp in length
175425: contig of 54847 bp in length
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                     ATTTTTAGTCTTTTCTTCTGAATTCATTACTTCCTTGTAGATAAGTTCTGTAAGAAACAG
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vector_side:right"
120479. .120578
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57142. .57241
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JOURNAL COMMENT
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AUTHORS
TITLE
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G49140/c
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                                                                                                                                                                                                                                                                                                                                                                                      Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TTTGTGTAGGGGTTGCAAGAAAT
Primer B: CCACATTGACTTGATGGTCAAAA
STS size: 282
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1 (bases 1 to 401)
Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., (
Unpublished (2000)
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SHGC-79840 Human Homo
G49140
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STS.
                                                                                                                                                                                                                                                                                                      Protocol:
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                      ends sequenced at TIGR from the RPCI11 developed at the Stanford Human Genome Location/Qualifiers
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KCl:
Tris-HCl:
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PCR Cycles:
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                                                                                                                   organism="Homo sapiens"
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49.7%;
99.5%;
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sapiens
Score 397.8; DB 7; Pred. No. 1.9e-111;
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RRS Muzny, D. Marie . Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Bardaranaike, D., Barber, M., Barastead, M., Benahmed, F., Badawin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Bardaria, M. L., Davia, C., Burch, P., Burrell, K., Cadderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Crox, C., Coyle, M., Cree, A., D'Souza, L., Cardenas, V., Chen, Z., Chu, J., Chen, R., Chen, Z., Chu, J., Chen, R., Chen, Z., Chu, J., Checkell, M. L., Davis, G., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draba, M., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Eggan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farls, M., Geer, M., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harlak, P., Hanes, A., Henderson, N., Hernandez, J., Hernandez, J., Hawes, A., Henderson, N., Hernandez, J., Harly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Xargathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Lovan, J., Lewis, L., Li, Z., Liu, J., Lovan, J., Lewis, L., Li, Z., Liu, J., Lovan, J., Lewis, L., Li, Z., Liu, J., Lovan, M., Mahindartne, M., Mahinda
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AC154950.2 GI:68265244
HTG; HTGS_PHASE1; HTGS_DRAFT;
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Bos taurus clone CH240-42G8,
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1 (bases 1 to 206504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
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L Submitted (01-UUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 28, 2005 this sequence version replaced gi:57164422.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projecte/rar/). Bach contig desgribed in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, L., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walson, R., Willson, R., Walczyk, R., Wooden, L., Walte, F., Williams, G., Willson, R., Waczen, R., Wei, X., Wooden, K., Woon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, X., Dunn, D., von, Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-JAN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 206504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            table.
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Direct Submission
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 29 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                Center project name: FCEU
Center clone name: CH240-4268
Center clone name: CH240-4268
Center clone name: CH2640-4268
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 195434 bases at least Q40
Consensus quality: 197609 bases at least Q30
Consensus quality: 199501 bases at least Q20
Consensus quality: 199501 bases at least Q20
Estimated insert size: 200872; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ Genome Center
Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
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                                     /estimated_length=unknown
6557. .6838
                                                                             /estimated_length=50
5784. .5883
                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-42G8"
                                                                                                                                                                                                                                     organism="Bos taurus"
                estimated_length=282
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of 3762 bp in length
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of 4118 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 2091 bp
871 bp
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12049 bp in length
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28282 bp in length
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20100 bp in length
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23248 bp in length
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yn length

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477; Conserv
       AC137121 181548 bp DNA linear ROD 16-OCT-2
Mus musculus chromosome 5, clone RP23-286M22, complete sequence.
AC137121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATTCÁAAAGGGCAAGGAGACTGAAATCATTAGAGGGAAACAGGTA-ATCTAACTGGTT 11824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCTCCACATTGACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCÂC
                                                                                                                                                                                                                                                                                                                           TTCATTACTTAATGCCAAATAATTACGTTTTTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTAAAGTTCTGAAAGAACTCATGCTAAATCATTATAGTCAGAATAAATGCCACACTAA 11765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCACCCTTTA----ATCAGATTATGCTAATATTTCTTCAAGATT---CTTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTACCCTTTAGCCCATGTTAACATTTTCTTCAGGATTCATTACTATTAAAATTATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACTCCACACTGAGGTGGTGAGAGAGGGCATTATGGATCTGAATTTTGATGAGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAGT---AAACTTTAGAGTGAATGAAGGAAAAGGTTTTTAGGTGGAGGGATTGATTCCT 11599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAGTTCAAACACTAAGAATGAATGAGGGAAGAGGT----AGCGGCTGAAAGGATTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTGTAACAAA-GGTACCAGTGTTATGAAAATCAGTTTTCTCCTTAACCCAAAGAAAAA
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14769. .14818
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Pred. No. 8.8e-61;
0; Mismatches 185;
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                                                                                  ROD 16-OCT-2004
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CE 3 (bases 1 to 181548)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Barra, N., Barra, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H. M., Barra, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H. M., Barra, N., Bastien, V., Anderson, M., Anderson, S., Cooke, P., Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Choepel, Y., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Caldymore, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Mahnova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Niec, S., Viel, R., Niec, S., Mander, A., and Zody, M., Nison, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Spencer, S., Schauer, S., Whissin, M., Talamas, J., Tesfaye, S., Theodore, J., Theodore, J., Mathodore, J., Mathodore, J., Mathodore, J., Wassiliev, H., Venk
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, M., Bastien, V., Anderson, M., Anderson, M., Boukhgalter, B., Camarata, J., Chang, J., Cheepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Galagan, J., Bardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacCean, C., Macdonald, P., Major, J., Manning, J., Mathhews, C., Murphy, T., Naylor, J., Nguyen, C., Mihova, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-AUG-2004) Whitehead Institute/MIT Center
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-OCT-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 16, 2004 this sequence version replaced gi:51315566. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence submissions@broad.mit.edu
------ Project Information
Center project name: L26408
Center clone name: 286_M_22
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6014. .6091
                                                                                                                                                                                                                                                                                                /rpt_family="AT_rich" complement(6312. .675)
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complement(1596. .1764)
/rpt_family="Tigger7"
plan_family="Tigger7"
                                                               complement (11814. .12121)
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648. .827
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/db_xref="taxon:10090"
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 CTGAATTCATTACTTCCTTGTAGATAAGTTCTGTA----AGAAACAGCTGTGTTATTATA 733
                                                                 GAGAGTGAGTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTT
                                                                                                 TATGACCACACCCGTCAAGGGCCTGAA-----AGACACGAGCTTCTTGGTTATTCACG
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30909. .30939
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/rpt family="MT2A"
29537. .29558
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complement(28452..28558)
/rpt_family="L2"
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complement(26526. .27115)
/rpt family="L1_MM"
27127
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/rpt_family="ORR1A2"
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21853. .21904
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15813. .25856
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/rpt_family="B3A"
25195. .25696
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20949. 21640
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14706. .14843
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20110. .20146
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Pred. No. 9.7e-24;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus
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Rattus norvegicus (Norway rat)
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On Apr 5, 2003 this sequence version replaced gi:28913313
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Consensus quality: 19161 bases at least Q40
Consensus quality: 195784 bases at least Q30
Consensus quality: 195987 bases at least Q30
Estimated insert size: 195646; sum-of-contigs estimation Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-140B2
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104621 contrig of 3442 bp in length
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115420 contrig of 6925 bp in length
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140452 contrig of 6102 bp in length
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PR 20-JAN-1999 FR 99/00586,26-FEB-1999 US 60/122175 PI
FRANCINE DESANLIS,ALAIN FOURNIER,ISABELLE MAURY,QING ZHOU LIU PC
C12N15/09,A61K39/395,A61K45/00,A61P7/10,A61P9/00,A61P25/00, PC
A61P25/14,A61P25/28,C07K16/40,C12N1/15,C12N1/19,C12N1/21 PC
PC A61P25/16,A61P25/28,C07K16/40,C12N1/15,C12N1/19,C12N1/21 PC
C12Q1/02,C12N9/12,
PC C12Q1/02,C12N9/12,
PC C12Q1/02,C12N1/48,C12N15/00,C12N5/00
CC POLYPETIONS DESCRIPTION OF THE COST OF THE 
Sequence 24 from patent
AR430630
AR430630.1 GI:40191471
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1 (bases 1 to 1422)

Desanlis F., Fournier, A., Maury, I. and Liu, Q.Z.

Polypeptides derived from JNK3

Patent: JP 2002534982-A 23 22-OCT-2002;
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OS Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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JP 2002534982-A/23
22-OCT-2002
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1. .1422
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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97.7%;
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Pred. No. 4e-14;
0; Mismatches
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US 6649388
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AX027295/c
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Best Local S
Matches 84
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 686 ATTACTTCCTTGTAGATAAGTTCTGT 711
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Sequence 24
AX027295
AX027295.1
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Fournier, A., Maury, I., Zhou-Liu, Q. ar Polypeptides derived from JNK3
Patent: US 6649388-A 24 18-NOV-2003;
Aventis Pharma S.A.; Antony;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                    GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 1224
                                                         GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC
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ilarity 97.7%;
Conservative
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/db_xref="GI:10188272"
/db_xref="GI:10188272"
/db_xref="GI:10188272"
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/translation="MSKSKVDMAPYSVEVTHKNIISLLNVFTPQKTLEEFQ
DAVLDRAVAIKKLSRPFQNQTHAKRAYRELVLMKCVUHKNIISLLNVFTPQKFTLEEFQ
DVYLVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKFSNIVVK
SDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILLGMGYKENVDIWSVGCIMGEM
VRHKILFFGRDYIQMNKVIEQLGTFCDEFMKKLQFTVRNYVENRPKYAGLTFFKLFF
DSLFFADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHBYINVMYDPARVEAFP
PGIYDKQLDEREHTIEEWKELIYKEVMNSEEKTKNGVVKGQPSPŞGAAVNSSESLPPS
SSVNDISSMSTDQTLASDTDSSLEASAGPLGCCR"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                         note="unnamed protein product"
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Pred. No. 4e-14;
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WO0043524.
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BD078044/c
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PN JP 20
PN 23-OC
PF 05-OC
PF 05-OC
PF 03-OC
PR ROGER
PI CHIA
PI DERK
PI CHIA
PI A61P2
PC A61P2
PC A61P2
PC A61P2
PC A61P3
PC A61
                                                                                                                             Homo sapiens (human)
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Sequence 56 from Patent
CQ892479
CQ892479.1 GI:55165021
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                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1505)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J.,
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Weihe, E.D., Schaefer, M.K.,
                                                     Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD078044
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C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROGER J DAVIS,RICHARD A FLAVELL,PASKO RAKIC,ALAN J WHITMARSH,CHIA YIN KUAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1998 JP 2000514991
03-OCT-1997 US 60/060995
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Key Location/Qualifiers
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JP 2001519146-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism='Unidentified'
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Pred. No. 3.9e-14;
0; Mismatches 2
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EP1469316.
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od of using the same.
     Gillen, C.,
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     Wetzels, I.
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                                                                                                                                                                                                                                                                                                     PAT 01-NOV-2004
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        Wnendt, S
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Matches 84; Conserv
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Sequence 1 from p
AR716219
AR716219.1 GI:77
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AR380407
Yang, D.D.

JNK3 modulators and methods of use Patent: US 6943000-A 1 13-SEP-2005;
                                                                                                                                                                                                                                                                                                                                                                                      Cocks, B.G., Stuart, S.G. and Seilhamer, J. Compositions for the detection of blood response gene expression patent: US 6607879-A 952 19-AUG-2003; Incyte Corporation; Palo Alto, CA
                             1 (bases 1 to 1505)
Davis,R.J., Flavell,R.A., Rakic,P.,
                                                        Unclassified
                                                                    Unknown
                                                                                Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
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Patent: EP 1469316-A
Gruenenthal GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
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                                                                                                                                                                                                              ATTACTTCCTTGTAGATAAGTTCTGT
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/mol_type="genomic DNA"
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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patent US 6943000
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Pred. No. 3.9e-14;
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Pred. No. 3.9e-14;
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US 6
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                                  Kuan, C.-Y.
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Matches 84
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                          AUTHORS
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Sequence
AX377861
           1 (bases 1 to 1505)
Gupta, S., Barrett, T.,
Derijard, B. and Davis,
                                                                                                                                                       HSU34819 1505 bp
Human JNK3 alpha2 protein kinase
 Selective interaction
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                         Homo sapiens
                                                                                                                                                U34819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening method
Patent: WO 0212338-A 56 14-FEB-2002;
Gruenenthal GmbH (DE)
                                                                                                         Homo sapiens (human)
                                                                                                                                   U34819.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gillen, C., Wetzels, I., Wnendt, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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1. .1505
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                                                                                                                                   GI:1463124
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/mol_type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:19573951
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97.7%;
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Pred. No. 3.9e
0; Mismatches
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                       Whitmarsh, A.J.,
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Pred. No. 3.9e-14;
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mRNA, co
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RESULT 17
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Collins, F. S., Wagner, L., Shemmen, C. M., Schulet, G. D.
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M. Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
                                                                                                                                                                                                                                                                                                                                                                                                                   1850 bp Homo sapiens mitogen-activated FIMAGE: 5721954).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (25-AUG-1995) Roger J. Davis, Molecular Medicine,
University of Massachusetts Medical School; 373 Plantation Street,
Worcester, MA 01605, USA
                                                                                                                                                                                                             Hominidae, Homo.

1 (bases 1 to 1850)
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  BC065516.1 GI:41350833
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EMBO J. 15 (11), 2760-2770 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSLHFLYYCSEPTLDVKIAFCQGFDKQVDVSYIAKHYNMSKSKV
DNQFYSVEVGDSTFTVLKRYQNLKFIGSGAQGIYCAAYDAVLDAVIKLLSRFPQNQ
THAKRAYRELVLMKCVNHKNIISLINVFTPQKTLEEFQDVYLVMELMDANLCQVIQNE
LDHERNSYLLYQMLCGIKLHHSAGIIHADLKPSNIVVKSDCTLKILDFGLARTAGTSF
MMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYIDQNNKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKÁSQARD
LLSKWLVIDPAKRISVDDALGHPYINVWYDPAEVEAPPGOIYDKQLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKKGQPSPSGAAVNSSESLPPSSSVNDISSMSTDQTLASDTD
SSLEASAGPLGCCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="UNK3 alpha2 protein kinase"
/protein_id="AAC50604.1"
/db_xref="GI:1463125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="UNK protein kinase isoform that phosphorylates the transcription factor c-Jun on Ser-63 and Ser-73; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="JNK3A2"
68. .1462
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="JNK3A2"
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protein kinase 10,
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3.9e-14;
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mRNA (cDNA clone
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RESULT 18 AK091104/c LOCUS

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2095 bp

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PRI 20-JAN-2006

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                                                  989
                                                                                                           939
                                                                                                                                                                    626
                                                                                                                                                                                                                         84;
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20986507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length burner and marraes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N.A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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Submitted (26-JAN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaithersburg, Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH MGC Project
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                          ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                        GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAATTC
                                                                                                                                            GTACCTGAAGGAGAGAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTTCTGAATTC
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                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Ovary, pooled from 3
/clone lib="NIH_MGC_125"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5721954"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                 10.3%;
97.7%;
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                                                                                                                                                                                                                                                 Score 82.8;
Pred. No. 3.
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854
                                                                                                                                                                                                                                     3.9e-14;
                                                                                                                                                                                                                                                                               Length 1850;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotute, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Satto, K., Nishikawa, T., Kimura, K., Matsuo, K., Kawai-Hio, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsum, M., Takahashi-Fujii, A., Oshima, A., Kugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Nugano, S., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T., Nagai, K., and T., and T.,
                                                               Submitted (04-JUL-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:flj-cdna@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction; Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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AK091104.1 GI:21749394
oligo capping; fis (full insert sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human cDNAs
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/organism="Homo sapiens'
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VERSION
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                                                                                                                                                            AUTHORS
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Query Match
Best Local Similarity
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JNK3-controller and method of using the same Patent: JP 2001519146-A 2 23-OCT-2001; UNIVERSITY OF MASSACHUSETTS
                                                                                                                                                                                                    JNK3-controller and method of using BD078045
                                                                        1 (bases 1 to 2366)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J.,
                                                                                                                                                                   BD078045.1 GI:22623648 JP 2001519146-A/2.
                                                                                                               unclassified
                                                                                                                                  unidentified
                                                                                                                                                    unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 2005109001-A 10 17-NOV-2005; Galapagos Genomics N.V. (BE); Spittaels,
                                                          Yang, D.D.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="substantia nigra"
/clone_lib="BRSSN2"
/note="cloning vector: pME18SFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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/db_xref="taxon:9606"
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Pred. No. 3.8e-14;
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Pred. No. 3.8e-14;
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                                                                           Kuan, C.Y. and
                                                                                                                                                                                                                                             PAT 27-AUG-2002
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Best Local Similarity

Matches 84; Conserv
                                                                                                              Matches
                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                      AR716220
Sequence
AR716220
                                                                                                                                                                                                                           JNK3 modulators and methods of use Patent: US 6943000-A 3 13-SEP-2005; University of Massachusetts and Yale University; Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified
                                                                                                                                                                                                                                                                                                                      Unknown.
                                                                                                                                                                                                                                                                              Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J.,
                                                                                                                                                                                                                                                                                                                                   Unknown.
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                                                                         GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                 ATTACTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROGER J DAVIS,RICHARD A FLAVELL,PASKO RAKIC,ALAN J WHITWARSH,CHIA YIN KUAN,
DERK DI YANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1998 JP 2000514991
03-OCT-1997 US 60/060995
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JP 2001519146-A/2
23-OCT-2001
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                       /organism="unknown"
/mol_type="genomic |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism='Unidentified'
                                                                                                                                                                                                                 Location/Qualifiers
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from patent US 6943000.
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                                                                                                           ; Score 82.8; DI
; Pred. No. 3.8e
0; Mismatches
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Pred. No. 3.8e
0; Mismatches
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                                                                                                                                                                             DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
.8e-14;
                                                                                                                          .8e-14;
                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                      <u>ب</u>
                                                                                                                                     Length 2367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2366;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                Kuan, C.-Y.
                                                                                                                                                                                                                                                                                                                                                                                                  PAT 07-OCT-2005
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                                                            1420
                                                                                     885
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AUTHORS
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BC051731/c
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                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:50974 IMAGE:4838495"
/tissue_type="Testis"
/clone_lib="NMH_MGC_97"
/lab_host="DH10B"
note="Vector: pBluescriptR"
                                                                                                              ocation/Qualifiers,
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RS Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Schen, S.J.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Betheeda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
through the I.M.A.G.E. Consortium/LLNL at: http://image.llrseries: IRAK Plate: 90 Row: k Column: 24
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiral Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 pp mRNA linear Homo sapiens mitogen-activated protein kinase 10, MGC:50974 IMAGE:4838495), complete cds.
                                                                                                                                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                           Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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     gi: 20986509
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TITLE
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              84;
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AR454561
AR454561.1
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Loring,J.F., Tingley,D.W. and Edwards,C.M.
Genes expressed in alzheimer's disease
Patent: US 6602888-A 34 27-JAN-2004;
Incyte Corporation; Palo Alto, CA
Location/Qualifiers
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                                                             ATTACTTCCTTGTAGATAAGTTCTTT 1710
                                                                                                                                                                                      GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAAfTC 1736
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LKESNIVKSDCTLKILDFGLARTAGTSFMMTFYUVTRYYRAFBYJICHGYKENVDMW 
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GLTFFKLFDDSLFPADSSHNKLKASQARDLLSKNLVIDPAKRISVDDALCHFYINVY 
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GLTFFKLFDDALCHFY 
GLTFFKLFDDALCHFY 
GLTFFKLFT 
GLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:42688030
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|xref="IMGT/GENE-DB:6872"
|xref="MIM:602897"
                                                                                                                                                                                                                                                                                                                                     10.3%;
97.7%;
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                                                                                                                                                                                                                                                                                                           Score 82.8; DB 2;
Pred. No. 3.7e-14;
0; Mismatches 2;
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Pred. No. 3.7e-14;
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RESULT 24

the following selection criteria: Location/Qualifiers

mRNA gi: 20986504

/organism="Homo sapiens"
/mol\_type="mRNA"
/db\_xref="taxon:9606"

clone="IMAGE:4792970"

note="Vector: pBluescript"

host="DH10B'

tissue\_type="Brain, hypothalamus" clone\_lib="NIH\_MGC\_96"

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REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBMED
REFERENCE
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KEYWORDS
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LOCUS
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,
Villalon, D.K., Muzny, D.M., Sodergren, F.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, F.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Mitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
p. 12477917
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 8
This clone was selected for full length sequencing because it
                                                                                                                                                                                       cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCU22492
Homo sapiens mitogen-activated p
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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mRNA (cDNA clone
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JOURNAL
PUBMED
REFERENCE
AUTHORS
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AUTHORS
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BC035057/c
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KEYWORDS
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Best Local S
Matches 84
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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CE 1 (bases 1 to 2690)

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

RTM Mammalian Gene Collection Program Team

Be human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                               Direct Submission
Submitted (31-UL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirak
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 73 Row: d Column: 6
This clone was selected for full length sequencing because it
                                                                                                                                                                      http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECU35057 2690 bp mRNA lir
Homo sapiens mitogen-activated protein kinase
MGC:41877 IMAGE:5261221), complete cds.
                                                                                    Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH MGC Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                            Stephanie Rodrigues,
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97.7%;
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Pred. No. 3.7e-14;
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                                                                                                                                            Amy Sanchez
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                                                                                                                                            Mark Ketteman, Anuradha
and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2678;
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mRNA (cDNA clone
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SOURCE
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CS206710/c
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                                                                                                                                                                                                    AUTHORS
JOURNAL
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                               Spittaels, K.F.
Patent: WO 2005109001-A 11 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 from Patent CS206710
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                              Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="MAPK10 protein"
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THAKKRYRELYUMKCVMHKNIISLLNVFTPQKTLEEFGDVYLLWMELMDANLCQVIQME
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LDHEERNSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTHACTS
MTFFYVTRYYRAFEVILGHGYKENVDIWSVGCIMGEMVRHILLFPERDYIDQMKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLEASAGPLGCCR"
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LLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
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                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIYKEVMNSEEKTKNGVVKGQPSPSGAAVNSSESLPPSSSVNDISSMSTDQTLASDTD
                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonyms: p493F12, p54bSAPK, JNK3A, FLJ12099,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="Brain, hippocampus"
/clone Tib="NIH MGC_95"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                   Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Kikuchi, H., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project
Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,
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Homo sapiens cDNA FLJ42801 fis, clone BRCAN2001223, highly
to MITOGEN-ACTIVATED PROTEIN KINASE 10 (EC 2.7.1.-).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                               Submitted (04 JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized step-codon. The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the DNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.
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Hines, L., Rolles, A., Jepson, D., Moreira, D., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Williamson, J. and LaBaer, J.
Direct Submission
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Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F. Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.
Cloning of human full-length CDS in Creator (TM) recombinational
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1269 bp mRNA linear SYN 22-MAR-2 Synthetic construct Homo sapiens clone FLH117970.01X mitogen-activated protein kinase 10 (MAPK10) mRNA, complete cds.
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/organism="synthetic construct"
/mol_type="mRNA"
                                                                                                                                            Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRCAN2001223"
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/clone_Tib="BRCAN2"
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Pred. No. 3.
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Zuo,D., Taycher,E.
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Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). The CDS has been directionally cloned using
BD In-Fusion(TM) cloning system between the SalI and HindIII sites
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
after SalI site and before 'ATG' to provide Kozak consensus
sequence; 'GG' after last codon and before HindIII site to maintain
reading frame. Each clone is clonally isolated and full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY890997 1269 bp mRNA linear SYN 21-MAR-2005
Synthetic construct Homo sapiens clone FLH020610.01L
mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.
                                                                                                                                                                                                                                                                         Submitted (05-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                      Hines,L., Rolfs,A., Jepson,D., Moreira,D., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Williamson,J. and LaBaer,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinnes,L., Rolfe,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F. Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and Labaer,J.
Cloning of human full-length CDS in Creator (TM) recombinational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct
synthetic construct
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Human ORF Project.
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/(codon_start=1)
/(codon_start=1)
/(codon_start=1)
/(product="mitogen-activated protein kinase 10"
/protein_id="mitogen-activated protein kinase 10"
/protein_id="max41509.1"
/db_xref="GI:61358132"
/(translation="MSLHFLYYCGEPTLDVKIAFCQGFDKQVDVSYIAKHYNMSKSKV
/translation="MSLHFLYYCGEPTLDVKIAFCQGFVCAAYDAVLDRNVAIKKLSRPEQNQ
THAKRAYRELVLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLGGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSF
MMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYIDQMNKVI
EQLCTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFDSLFPALSEHNKLKASQARD
LLSKMLVIDPAKRISVDDALQHPYINVMYDDAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKGQPSPSAGVQQ"
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note="derived from Homo sapiens first strand cDNA library
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98.8%;
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Direct Submission
Submitted (05-JAN-2005) Biological Chemistry and Molecular Submitted (05-JAN-2005) Biological Chemistry and Molecular Stabmitted (05-JAN-2005) Biological Chemistry and 
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Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and LaBaer, J.
Cloning of human full-length CDS in Creator (TM) recombinational
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Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelle
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.
Williamson, J. and LaBaer, J.
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DNQFYSVEVGGSTFTYLKRYQNLKPIGSGAQGIVCAAYDAVLDRINAIKKLSRPFQNG
THAKRAYRELVLMKCVHKNIISLLAVFTPQKTLEEFQDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLCGIKHLKSAGIIHRDLKPSNIIVVKSDCTLKILDFQLARTAGTSF
MMTPYVTRYXRAPEVILGMCKENVDIWSVGCIMGEMVRHKILFPGADXEHKKLASAGARD
EOLGTPCPEEFMKKLQDTVRNYVENRFXYAGLTFPKLFPDSLEHKLKASAGARD
LLSKMLVIDPAKRISVDDALQHPYINVMYDPAEVEAPPPQIYDKQLDEREHTIEEMKE
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/protein_id="AAX42931.1"
/db_xref="GI:61366953"
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/transl_table=11
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//ab_host="Bscherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
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Pred. No. 2.2e-13;
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Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and
                                                                                                                                                                             2 (bases 1 to 1269)
Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J.,
Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
Direct Submission
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Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
Cloning of human full-length CDS FLEXGene in
Gateway (TM) recombinational vector system
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Synthetic construct Homo sapiens clone FLH057665.01X
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/protein id="AAX43143.1"
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/bccefing1:611368268"
/translation="MSLHFLYYCSEPTLDVKIAFCQGFDKQDDVSYIAKHYNMSKSKV
/translation="MSLHFLYYCSEPTLDVKIAFCQGFDKQDDVSYIAKHYNMSKSKV
DNQFYSVEVODSTFTYVLKRYQNLKFIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFONQ
THAKRAYRELVLMKCVUNHKNIISLLNUFTPQKTLEBFQDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSF
MMTPYVVTRYYRAPBVILGMGYKENVDIMSVGCIMGENVRHKILFPGRDYIDQMNKVI
BQLGTPGPBFMKKLQPTVRNYVENRFKYAGLTFPKLFFDSLFFADSEHNKLKASQARD
LLSKMLVJDBAKRISVDALGHGYINNWYDPAEVEAPPPQIYDKQLDEREHTIEEMKE
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note="derived from Homo sapiens first strand cDNA
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Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fus
                                                                                                                                                    Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J. Direct Submission
                                                                                                    Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
                                                                                                                                                                                                                                                    Gateway (TM) recombinational vector system Unpublished
                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1269)
Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J.,
Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
Cloning of human full-length CDS FLEXGene in
                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic construct synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY893752 1269 bp mRNA linear 9
Synthetic construct Homo sapiens clone FLH057664.01L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY893752.1 GI:60827196
Human ORF Project.
                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitogen-activated protein kinase 10 (MAPKIO) mRNA,
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/trans| table=11
/product="mitogen-activated protein kinase 10"
/product="mitogen-activated protein kinase 10"
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/protein_id="AAX36339.1"
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/db_xref="GI:60815281"
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NQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLLRNVAIKKLSRFFQNQ
THAKRAYRELVLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQME
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIIVKSDCTLKILDFGLARTAGTSF
MMTPYVVTRYYKAFEVILGMGYXENVDIWSVGCIMGEMVRHKILFFGRDYIDQNMVL
EQLGTPCPEFMKKLQFTVRNVYENRFKYAGLTFFKLFPDSLFRASSHNKLKASQARD
EQLGTPCPEFMKKLQFTVRNVYENRFKYAGLTFFKLFPDSLFRASSHNKLKASQARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ"
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/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
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/mol_type="mRNA"
/db_xref="taxon:32630"
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Pred. No. 2.2e-13;
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allow fusion

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BT019710/c
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                                                     JOURNAL
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Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein, Koundinga,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin, Phelan,M. and Farmer,A.

Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                     BT019710 1269 bp mRNA linear SYN 28-OCT-200 Synthetic construct Homo sapiens mitogen-activated protein kinase 10 mRNA, partial cds.
BT019710 BT019710 GI:54696287
FII CONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
Submitted (28-OCT-2004) BD Biosciences Clontech, 1020 East Meadow circle, Palo Alto, California 94303, USA
This CDS clone is a part of a collection of human full length
                                                                       2 (bases 1 to 1269)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                              synthetic construct
synthetic construct
other sequences; artificial sequences
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                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                            vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Codon_start=1
/trans1_table=11
/trans1_table=11
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/protein id="nAX36789.1"
/db_xref="GI:60827197"
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LDHERMSYLLYQMLGGIKHLHSAGIHRDLKPSNIVVKSDCTHKILDFGLARTAGTSF
MMTPYVVTTRYFRAPEVILGMGYKENVDIMSCIMGEMVRHKILFPGRDYIDQMNKVI
EQLCTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPALDSEHNKLKASQARD
LLSKMLVIDPAKRISVDDALQHPYINVMYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKGQPSPSAQVQQD"
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note="derived from Homo sapiens first strand cDNA library
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Pred. No. 2.2e-13;
0; Mismatches 1;
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BD249786/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81;
                                                                                                                                                              Hominidae; Homo.

1 (bases 1 to 1306)

Desanlis, F., Fournier, A., Maury, I. and Liu, O.Z.

Polypeptides derived from JNK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the DNR-DDAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
PR 20-JAN-1999 FR 99/00586,26-FEB-1999 US 60/122175 PI FRANCINE DESANLIS,ALAIN FOURNIER,ISABELLE MAURY,QING ZHOU LIU PC C12N15/09,A61K39/395,A61K45/00,A61P7/10,A61P9/00,A61P25/00, PC
                                      PR PR
                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                             BD249786.1 GI:33059556
JP 2002534982-A/22
                                                                                                                             Patent: JP 200253
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 Polypeptides derived from JNK3.
BD249786
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                                                                      Homo sapiens (human) JP 2002534982-A/22 22-OCT-2002
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                                      19-JAN-2000 JP 2000594932
20-JAN-1999 FR 99/0058
                                                                                                                                                JP 2002534982-A 22
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collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIYKEVMNSEEKTKNGVVKGQPSPSAQVQQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="mitogen-activated protein kinase
/protein_id="AAV38516.1"
/db_xref="GI:54696288"
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/db_xref="taxon:32630"
/clone="GH01307L1.0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
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Pred. No. 2.2e-13
                                                                                                                                                                                                                                                                                                                                                                                       1306 bp
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AX027293/c
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Sequence
AR430629
AR430629.
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Sequence 22 from Patent
AX027293
AX027293.1 GI:10188269
                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1306)
Fournier, A., Maury, I., Zhou-Liu, Q. at
Polypeptides derived from JNK3
Patent: US 6649388-A 22 18-NOV-2003;
Aventis Pharma S.A.; Antony;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81;
                         Homo sapiens (human)
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PC A61P25/16, A61P25/28, C07K16/40, C12N1/15, C12N1/19, C12N1/21
C12N5/10, C12N9/12,
PC C12Q1/02, C12Q1/48, C12N15/00, C12N5/00
CC Polypeptides derived from JNK3
FH Key Location/Qualifiers
FT CDS (142) (1201)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                       Similarity
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CDS (142) (1293)
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1. .1306
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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Pred. No. 2.2e-13;
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Pred. No. 2.2e-13;
D; Mismatches 1
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BD078046/c
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JNKS-controller and method of using the same Patent: JP 2001519146-A 3 23-OCT-2001;

UNIVERSITY OF MASSACHUSETTS

OS Unidentified
PN JP 2001519146-A/3
PD 23-OCT-2001
PF 05-OCT-1998 JP 2000514991
PF 03-OCT-1997 US 60/060995
PR 03-OCT-1998 UP 60/060995
PR 03-OCT-2001
PR 03-OCT-201
PR 03-OCT-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unclassified sequences.
1 (bases 1 to 1773)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.
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BD078046.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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C12N15/09, A01K67/027, A61K31/711, A61K45/00, A61K48/00, A61P9/10,
A61P21/00,
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/db_xref="GI:10188270"
/db_xref="GI:10188270"
/traislation="MSKSKUDNGFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAY
/traislation="MSKSKUDNGFYSVEVGUSTFTVLKRYQNLKPIGSGAQGIVCAAY
DAVLDRNVAIKKLSRPFQNGTHAKRAYRELVLMKCVNHKNIISLLAVFTPQKTLEEFQ
DYYLWELMDANLCQVIQMELDHERMSYLVTRYYAPEVILGMYXEMVDIWSVGCIMSEK
SDCTLKILDFGLARTAGISFMYTPYVTRYYAPEVILGMYXEMVDIWSVGCIMSEK
SDCTLKILDFGRDYIDQMNKVIEQLGTPCPEFMKKLQPTVRNYVENRFKYAGLTFPKLFP
WRHKILFPGRDYIDQMNKVIEQLGTPCPEFMKKLQPTVRNYVENRFKYAGLTFPKLFP
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PQIYDKQLDEREHTIEEWKELIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ"
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98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                         A FLAVELL, PASKO RAKIC, ALAN
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81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening method
Patent: EP 1469316-A 54 20-OCT-2004;
Gruenenthal GmbH (DE)
Yang, D.D.

JNK3 modulators and methods of use Patent: US 6943000-A 4 13-SEP-2005;
                                    Unclassified.
1 (bases 1 to 1773)
Davis,R.J., Flavell,R.A., Rakic,P.,
                                                                                                                                                     AR716221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                             Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weihe, E.D., Schaefer, M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Location/Qualifiers
1...1773
                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="unassigned DN/
/db_xref="taxon:9606"
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1. .1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                       from patent US
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                                                                                                                  GI:77364282
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Pred. No. 2.1e-13;
0; Mismatches 1;
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                                       Kuan, C.-Y.
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1 (bases 1 to 1773)
Gupta,S., Barrett,T.,
Derijard,B. and Davis,
Selective interaction
                                                                                          Homo sapiens (human)
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Human JNK3 alphal protein kinase
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Sequence 54 from Patent
AX377859
                                                    Hominidae; Homo.
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
                                                                                                                                                U34820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening method Patent: WO 0212338-A 54 14-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
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                                                                                                                                  GI:1463126
                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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ļ. .1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
/mol_type="genomic |
                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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Pred. No. 2.1e-13;
0; Mismatches 1;
 of JNK protein
                       Whitmarsh, A.J., Cavanagh, J., Sluss, H
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Pred. No. 2.1e-13;
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Sequence 345 from Patent
CQ714411
CQ714411.1 GI:42275268
                                                              Patent: WO 02068579-A 345 06-SEP-2002; PE Corporation (NY) (US)
                                                                                               thereot
                                                                                                              Kits, such as nucleic acid humanexons or transcripts,
                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-AUG-1995) Roger J. Davis, Molecular Medicine, University of Massachusetts Medical School, 373 Plantation Street, Worcester, MA 01605, USA
Derijard, B. Cell 76, 1025-1037, 1994
Sluss, H. K. Mol. Cell. Biol. 14, 8376-8384, 1994.
Location/Qualifiers
                                                                                                                                Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a
                                                                                                                                                                                Hominidae; Homo.
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EMBO J. 15 (11), 2760-2770
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DNQFYSYBVGDSTFTVLKRYQNLKFIGSGAQGIVCAAYDAVLDRUVAIKKLSRFFQNQ
THAKRAYRELVLMKCYNKKNIISLLNVFTPGKTLEEFQDVYLVMELMDANLCQVIQM
LDHERMSYLLYQMLCGIIGHLHSAGIIHBDLKPSNIVVKSDCTLKILDFGLARTAGTSF
LDHERMSYLLYQMLCGIIGHLHSAGIIHBDLKPSNIVVKSDCTLKILDFGLARTAGTSF
MTPYVVTRYYRAPEVILGMGYKENVDIMSVGCIMGEMVRHKILFGRBDYIDOMNKVI
EQUETPCPEFMKKLQPTVRNYVENRPKYAGLTFFKLFPDSLFPADSEHNKLKASQARD
LLSKMLVIIDPAKRISVDDALQHFYINVMYDDPADVEAPPPQIYDKQLDEREHTIEEMKE
LIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ"
/organism="Homo sapiens"
/mol_type="unassigned DNA"
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="UNK protein kinase isoform that phosphorylates the transcription factor c-Jun on Ser-63 and Ser-73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="JNK3 alpha1 protein kinase"
/protein_id="AAC50605.1"
/db_xref="GI:1463127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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WO02068579.
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                                                                                                                    for
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                                                                                                              detecting
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                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                              ising a majority expression and o
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                                                                                                                                                                                                  Catarrhini;
                                                                                                                                                                                                                 Euteleostomi;
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other uses
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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CS206711/c
LOCUS
                                                                                                               REFERENCE
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AUTHORS
TITLE
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ORGANISM
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ACCESSION
VERSION
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                                                                                   AUTHORS
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
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Sequence
AR709626
                                                                   Spittaels, K.F.
Patent: WO 2005109001-A 12 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels,
                                                                                                                                                                                                                        Sequence 12
CS206711
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                    CS206711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2131)
Levino, Z. and Bernstein, J.
Variants of protein kinases
Patent: US 6936450-A 87 30-AUG-2005;
                                                                                                                                                                                                             CS206711.1 GI:83412266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compugen Ltd.; Tel
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                                                                                                                                                                                                                                                                                                                                            CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                              CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                        CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCTTGTAGATAAGTTCTTT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                         Location/Qualifiers
1. 2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2131 bp
from patent US 6936450.
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Pred. No. 2.1e-13;
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Pred. No. 2.1e-13;
0; Mismatches 1;
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WO2005109001
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                                                                        Koenraad Frederick F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2131;
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AK057723/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irié, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishil, S., Yamamoto, J., Salto, K., Kawai, Y., Isono, Y., Nakamura, Y., Ishil, S., Yamamoto, J., Salto, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Kikkawa, K., Pujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi, F., Hara, H., Tanase, T.O., Nomura, Y., Togiya, S., Komai, F., Hara, R., Fakeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shimizu, F., Wakebe, H., Hishigaki, H., Satoh, N., Takahai, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sugiyama, A., Takemoto, M., Makagawa, S., Senoh, A., Mizoguchi, H., Gakhi, S., Pukuzuni, Y., Fujimori, Y., Komiyama, M., Tanigami, A., Pujiwara, T., Ono, T., Yamada, K., Pujii, Y., Ozaki, K., Hitao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Itakura, S., Pukuzuni, Y., Kawabata, A., Hikiji, T., Kobatake, N., Nagaima, Y., Shigata, M., Sasaki, M., Togashi, T., Oyama, M., Takahashi, Y., Sakaki, M., Togashi, T., Kobatake, N., Satoh, T., Shigata, M., Sasaki, M., Sasaki, M., Sasaki, M., Sasaki, T., Oyama, M., Takahashi, Y., Kakashashi, Y., Nasahita, R., Yamashita, R., Yada, T., Nakamura, Y., Takahashi, Y., Nasahita, R., Somora, M., Sasaki, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T., Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R., Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S., Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishi1,S., Yamamoto,J., Isono,Y., Sato,H., Xakai,HiO,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Similarity 98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                             Genet. 36 (1), 40-45 (2004)
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Pred. No. 2.1e-13;
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Patent: JP 2001519146-A 4 23-OCT-2001;
UNIVERSITY OF MASSACHUSETTS

OS Unidentified
PN JP 2001519146-A/4
PD 23-OCT-2001
PF 05-OCT-1998 JP 2000514991
PR 03-OCT-1997 US 60/060995
PI ROGER J DAVIS,RICHARD A FLAVELL,PASK
PI CHIA YIN KUNN,
PI DERK DI YANG
PC C12N15/09,A01K67/027,A61K31/711,A61K
PC A61P21/00,
PC A61P21/00,
PC A61P21/00,
PC A61P25/08,A61P25/14,A61P25/16,A61P25
PC G01N33/15,G01N33/50,C12N15/00,C12N5/
PC G01N33/15,G01N33/50,C12N15/00,C12N5/
PC Topology: Linear;
CC JNK3-controller and method of using
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Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:flj-cdna@nifty.com, Tel:81-438-52-3986)
REDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center. National Institute of Technology and
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JNK3-controller and method of using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unclassified sequences.
1 (bases 1 to 2372)
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NEDO human cDNA sequencing
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         Topology: Linear;
JNK3-controller and method of using the same
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C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
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03-OCT-1997 US 60/060995
ROGER J DAVIS,RICHARD A FLAVELL, PASKO RAKIC,ALAN
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/tissue_type="uterus"
/clone_lib="UTERU2"
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/db_xref="taxon:9606"
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BD078048.1 GI:22623651
JP 2001519146-A/5.
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JNK3-controller and method of
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1 (bases 1 to 2372)
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                                                                                                                                             10.1%;
llarity 98.8%;
Conservative
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03-OCT-1997 US 60/060995
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 2.1e-13;
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D; Mismatches 1
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                                                                                                                                                                                  Unclassified.

Unclassified.

1 (bases 1 to 2372)

Au-Young, J. and Seilhamer, J.J.

Composition for the detection of signaling pathway gene expression

Patent: US 6500938-A 1389 31-DEC-2002;

Patent: US 6500938-A 1389 31-DEC-2002;
                                                                                                                                                                                                                                                                                                                                       AR270826
Sequence
AR270826
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Patent: WO 2005109001-A 9 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                       CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                    CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAATTCATTA 689
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                                                                                                                                               /organism="unknown"
/mol_type="genomic DNA"
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/db_xref="taxon:9606"
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from patent US
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Search completed: July 19, 2006, 20:10:46 Job time : 5076 secs
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                                                                                                                        1415 CTTCCTTGTAGATAAGTTCTTT 1394
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Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 2372)
1 (bases 1 to 2372)
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.-Y. and Yang,D.D.
JNK3 modulators and methods of use Patent: US 6943000-A 6 13-SEP-2005;
University of Massachusetts and Yale University; Boston, MA
Location/Qualifiers
1. 2372
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                                                                                690 CTTCCTTGTAGATAAGTTCTGT 711
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Sequence 6 from patent US 6943000.
AR716222
AR716222.1 GI:77364283
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Maximum
Listing
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                                                                                                           AACCGGAGCCCATCTTGGTAGATGTTTCAACTATTGTCACATCAACCTTGAGAAGAGTTC
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Pred. No. 2.9e-171;
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                                                                                                                                                                                                                                                                                                                 SNP detection; breast tumor; endocrine disease; gynecology and obstetrics; neoplasm; cycostatic gene therapy; RNA interference; chromosome 4; d single nucleotide polymorphism; mitogen-activat Jun N terminal kinase-3; MAPKIO.
                                                                                                                 24-JUL-2003; 2003US-0490234P
25-NOV-2003; 2003US-00723681
25-NOV-2003; 2003US-0525239P
Identifying risk of, preventing and/or treating breast identifying and/or analyzing polymorphic variations in
                                   WPI; 2005-163257/17
                                                        Roth RB, Nelson MR, Hoyal-Wrightson CR;
                                                                                                                                                              27-MAY-2004; 2004WO-US016939
                                                                                                                                                                                                                                                          variation
                                                                                                                                                                                       17-FEB-2005
                                                                                                                                                                                                             WO2005014846-A2
                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                          (SEQU-) SEQUENOM INC
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/standard_name= "Single
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                                                                     Kammerer
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                                                                                                                                                                                                                                   nucleotide polymorphism
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                                                                                                                                                                                                                                                                                                                             protein kinase
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cancer by nucleotide
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RESULT 4
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Uma
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KW Gene
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Best Local S
Matches 464
                                                     SNP detection; breast tumor; controlled in gynecology and obstetrics; neoplasm; cytostatic; m gene therapy; RNA interference; chromosome 4; ds; single nucleotide polymorphism; mitogen-activated Jun N terminal kinase-3; MAPKIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for institutional polymorphic variation associated with breast cancer. The method of the polymorphic variation associated with breast cancer. The method of the invention demonstrates cytostatic activity and may be useful for identifying a risk of, preventing and/or treating breast cancer and cancer metastasis. The methods may be utilized for gene therapy or RNA interference. The current sequence is that of the human mitogen-activated protein kinase 10 (MAPKIO) SNP-containing gDNA MAPKIO-AC of the invention which is located at chromosome 4q22.1-q23.
Key
variation
                                            Homo
                                                                                                                                                           Human mitogen-activated
                                                                                                                                                                                         05-MAY-2005
                                                                                                                                                                                                                                                 ADY03501 standard;
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Pred. No. 1.5e-95;
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Matches 464;
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25-NOV-2003;
25-NOV-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for identifying a subject at risk of breast cancer comprising detecting the presence or absence of a polymorphic variation associated with breast cancer. The method of the invention demonstrates cytostatic activity and may be useful for identifying a risk of, preventing and/or treating breast cancer and cancer metastasis. The methods may be utilized for gene therapy or RNA interference. The current sequence is that of the human mitogen-activated protein kinase 10 (MAPKIO) SNP-containing gDNA MAPKIO-AD of the invention which is located at chromosome 4q22.1-q23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoyal-Wrightson
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                                                                                                                                GAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTCATTACTTCCT
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CACAGGGAAATTCATTACTTAATGCCAAATAATTACGTTTTGATG
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                                                          TGTAGATAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAAATTTATCCTTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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2003US-00723681.
2003US-0525239P.
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/standard_name= "Single nucleotide polymorphism
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Pred. No. 1.
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Best Local S
Matches 84
JNK3; c-jun N-terminal kinase 3; JNK3alphal isoform; JNK3alpha2 isoform;
                                                                                              07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1281 BP; 390 A; 297 C; 305 G; 289 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a process for preparing recombinant stre activated protein kinase b (SAPK b) using Escherichia coli. This encodes a recombinant stress-activated protein kinase b associate
                                            DNA encoding c-jun N-terminal kinase 3 derivative JNK3deltaNalpha2
                                                                                                                                             AAA59380
                                                                                                                                                                                          AAA59380 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Process for preparing recombinant stress-activated protein kinase b (SAPK b) using Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding recombinant stress-activated
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/note= "Recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9pp; Korean.
                                                                                                                                                                                          DNA;
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Pred. No. 5.8e
0; Mismatches
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RESULT 7 AAX37266/c ID AAX37266

standard;

DNA; 1505

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AAX37266; 20-MAR-2003 21-JUL-1999

(revised)
(first entry)

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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                      Sequence 1422 BP; 436 A; 322 C; 329 G; 335 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitogen-activated kinase; neurodegeneration; apoptosis; neuron; neurodegenerative disease; Alzheimer's; Parkinson's; brain injury; Huntington's disease; aging; acquired immune deficiency syndrome; cerebral anoxia; hypoxia; edema; gene therapy; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New derivatives of c-jun
ligands for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
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26-FEB-1999;
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                                                                                                                                                                                                                              Local Similarity
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1223
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                                                                                               GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACATTTTTAGTCTTTTTCTGAATTC
                                                                                                                                                    GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
ATTACTTCCTTGTAGATAAGTTCTTT
                                             ATTACTTCCTTGTAGATAAGTTCTGT
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fournier
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99US-0122175P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "JNK3deltaNalpha2"
                                                                                                                                                                                                                            10.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal kinase 3, useful for identifying neurodegeneration, have specific deletions
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RESULT 8
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BXXX
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for identifying compounds that modulate CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method CC comprises (a) incubating a cell that can express a JNK3 protein, or that CC has JNK3 activity, with a compound under conditions and for a time CC sufficient for the cell to express a JNK3 protein/activity without the CC compound; (b) incubating a control cell under the same conditions and for the same time without the compound; (c) measuring JNK3 expression/activity in the cell in the presence of the compound; (d) comparing the CC amount of JNK3 expression/activity in the presence and absence of the compound, where a difference in the level of expression/activity. The CC invention also provides a transgenic non-human mammal having a transgene CC disrupting expression of a JNK3 gene, the transgene being chromosomally CC integrated into germ cells of the mammal. JNK3 expression inhibitoris, e.g. antisense nucleic acids, are used to treat disorders involving; CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, Parkinson's CC disaupting expression sclerosis, trauma, motorneuron disease, Parkinson's CC disease or epilepsy. The present sequence represents the nucleic acid CC disease or chuman JNK3 (Genhank Acca No: UJ4819). JNK3 sequences under CC GenBank accession numbers UJ4820, U07620, L27128, L35236, X12740 and CC V0727 can also be used in the method of the invention. (Updated on 20-
                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches ·84
                                                                                                                                                                                                                                                                                                                                               Sequence 1505 BP;
16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY09200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-Jun N-terminal kina Alzheimer's disease;
                               ABL88412;
                                                                ABL88412 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1A; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification of c-Jun N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; disorder; Alzheimer's disease; Huntington disease; amyotrophic lateral sclerosis; ischemia; trauma; motorneuron disease; Parkinson's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic
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                                                                                                                                                 ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                                                                                                                                                                                                    GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                  correct
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of JNK3 (GenBank Accn No: U34819).
(first entry)
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                                                                                                                                                                                                                                                                                                                                               459 A; 343 C;
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                                                                                                                                                                                                                                                                                             10.3%;
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Pred. No. 6e-0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 357
                                                                                                                                                                                                                                                                                               6e-09;
                                                                                                                                                                                                                                                                                                               DB 2; Length 1505;
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RESULT 9
ADI31626/C
ID ADI316
XX
AC ADI316
XX
T1-JUN
T1 17-JUN
XX
Human
XX
KW Human;
KW Crohn'
KW irrita
KW acute
KW acute

(first

standard;

cDNA; 1505

ВP

1264 685 0

Human cDNA #952 17-JUN-2004 ADI31626; ADI31626

Human; gene; ss; immunological response; immunopathological condition; crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;

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Best Local Similarity
                                                                                                                                                                                                   The invention relates to identifying pain-regulating substances (A) comprises (i) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analyssic activity. (A) along with nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB8506-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention
                                                                                                                                                                            Sequence 1505
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000; 2000DE-01037759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2001; 2001WO-EP009011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200212338-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2002
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1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulated cDNA sequence
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                 ATTACTTCCTTGTAGATAAGTTCTGT
                                                                             GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 34; 213pp; German.
ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                         GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wetzels I,
                                                                                                                  Conservative
                                                                                                                                                                             B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; neurological disorder;
e disease; gene; ss.
                                                                                                                                                                             459 A; 343 C;
                                                                                                                               10.3%;
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                                                                                                                  0;
                                                                                                                  Score 82.8; D
Pred. No. 6e-0
0; Mismatches
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                           711
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                                                                                                                                                                               U; 0 Other;
                                                                                                                                                Length 1505;
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ADS83693/c
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches 84
                                                                     ADS83693 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-895307/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-1998;
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                                                                                                                                                                                                                                                                                            GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 952; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00023655
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                                                                     CDNA;
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Pred. No. 6e-09;
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ADS83693

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RESULT 11
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Best Local S
Matches 84
amyloid-beta precursor protein; pharmaceutical;
mitogen activated protein-kinase inhibitor; neu
                                              Human MAPK10,
                                                                                                                                          AEG09274 standard; DNA; 2211
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a human lymph node cDNA used to detect blood cell and immunological response gene expression. Note: The present sequence does not appear in the printed specification but was obtained in electronic format from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunopathological conditions, such as AIDS, allergies, anaemia, asthma, atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides which are used as probes to detect genes differentially expressed in an immunological response, abundantly expressed in an immunological response and/or coding for a polypeptide known to regulate blood cell biology. The polynucleotides are useful in research and diagnostic applications particularly in cancer and install in research and diagnostic applications particularly in cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaems; asthma; atherosclerosis; bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (seqdata.uspto.gov/sequence.html?DocID=20040077003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymph node cDNA #952
                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                       GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC
                                                                                                                                                                                                                                           ATTACTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                      GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                        ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stuart SG,
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                              (first entry)
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                                             transcript variant 2
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                                                                                                                                                                                                                                                                                                                                                                 10.3%;
97.7%;
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Pred. No. 6e-0
0; Mismatches
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                                                DNA
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neurological disease;
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mitogen activated protein-kinase inhibitor in admixture with a carrier.

The method involves activation of a biological pathway producing an indicator of the processing of amyloid-beta precursor protein e.g. a indicator of the processing of amyloid-beta precursor protein e.g. a composition of a reporter e.g. alkaline phosphatase, of phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The indicator induces the expression of a reporter e.g. alkaline phosphatase, of the pharmaceutical composition further comprises a label indicating use of the composition for treating or preventing a condition involving cognitive impairment or a susceptibility to the condition. The agent is useful in the manufacture of a medicament for inhibiting the processing of amyloid-beta precursor protein in a subject suffering from or susceptible to the abnormal processing of the protein, or for treating or preventing a condition involving cognitive impairment or a susceptibility to the condition, preferably, Alzheimer's disease. This sequence encodes human mitogen-activated protein kinase 10 (MAPKIO), transcript variant 2, a kinase involved in the up-regulation of amyloid-beta 1-42.
                                                                                                              Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel method of identifying a compound that inhibits the processing of amyloid-beta precursor protein in a mammalian cell. The invention also describes; a) an agent for inhibiting amyloid-beta precursor processing consisting of an antisense polynucleotide; a ribozyme or a small interfering RNA (siRNA), where the agent comprises a nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence encoding the polypeptide comprising the amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical; composition comprising the agent for inhibiting amyloid-beta precursor processing on an amyloid-beta precursor processing-inhibiting amount of a pharmaceutical in the polypeptide of a p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
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                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2006-231019/24
P-PSDB; AEG09283.
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24-AUG-2004; 2004US-0603948P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spittaels KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-2005; 2005WO-EP052182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective; Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GALA-) GALAPAGOS GENOMICS NV
(LAEN/) LAENEN W.
                                                                                                                                                                 Similarity
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Conservative
                                                                                                                                                                                                                                                                                                              B₽;
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transcript variant 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                         674 A; 498
                                                                                                                                                            10.3%;
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Pred. No. 6
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GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAATTC

Conservative

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Indels

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Gaps

GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC

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RESULT 12
AAX37267/G
ID AAX37
XX AAX37
XX AAX37
XX DT 20-MA
DT 20-MA
DT 21-JU
XX C-Jun
KW C-Jun
KW Alzhe
KW human
XX Homo
XX Discl
XX 
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                                                                                                                                                                                                   The invention relates to a method for identifying compounds that modulate CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method CC comprises (a) incubating a cell that can express a JNK3 protein, or that CC sufficient for the cell to express a JNK3 protein and for a time CC sufficient for the cell to express a JNK3 protein/activity without the CC compound; (b) incubating a comprol cell under the same conditions and for activity in the cell in the presence of the compound; (c) measuring JNK3 expression/ CC activity in the cell in the presence of the compound; (d) comparing the CC amount of JNK3 expression/activity in the presence and absence of the compound, where a difference in the level of expression/activity. The CC indicates that the compound modulates JNK3 expression/activity. The CC integrated into germ cells of the mammal having a transgene CC disrupting expression of a JNK3 gene, the transgene being chromosomally integrated into germ cells of the mammal JNK3 expression inhibitors, CC e.g. antisense nucleic acids, are used to treat disorders involving capture points and sease, Huntington disease, ischemia, amyotrophic lateral sclerosis, trauma, mocorneuron disease, Parkinson's CC disease or epilepsy. JNK3 sequences under GenBank accession numbers CC the method of the invention. (Updated on 20-MAR-2003 to correct DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
Query Match
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Matches 84
                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1C; 88pp;
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21-JUL-1999
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                            Local Similarity
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                                                                                                                           BP;
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                                                                                                                           712 A;
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                            10.3%;
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Score 82.8; DB 2;
Pred. No. 6.6e-09;
0; Mismatches 2;
                                                                                                                           C; 518
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RESULT 13
ADI61666/c
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                                       RESULT 14
AEA43831/c
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                                                                                                                                                                                                               Query Match
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Matches 84
                                                                                                                                                                                                                                                                                             The invention relates to a new composition comprising ADI61633-ADI61770and their complements that are cDNAs differentially expressed in brain disorders. Also included are a high throughput method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids and a high throughput method for screening a library of molecules or compounds to identify a ligand that specifically binds a cDNA. The expression of the each of the cDNAs is downregulated at least two-fold in the brain of the subjects with Alzheimer's disease (ADI61633-ADI61727) or upregulated at least two fold in Alzheimer's disease. (ADI61727) or upregulated at least two fold in For diagnosing or treating Alzheimer's disease. The present sequence is a cDNA downregulated at least two-fold in the brain of the subjects with Alzheimer's disease.
AEA43831;
                         AEA43831 standard; cDNA; 2677
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 34; 223pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising cDNAs that are differentially expressed in brain disorders, useful for diagnosing or treating Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-118572/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-2000; 2000US-00566921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA downregulated in Alzheimer's disease, INCYTE 413797.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI61666 standard; cDNA; 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-2000; 2000US-00566921
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                                                                                                                                                     989
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                                                                                                                                                                                                                   84.
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                          2677
                                                                                                 ATTACTTCCTTGTAGATAAGTTCTTT 1710
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                                                                                                                         ATTACTTCCTTGTAGATAAGTTCTGT
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                         BP; 785 A; 598 C;
                                                                                                                                                                                                                             10.3%;
97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edwards CM;
                                                                                                                                                                                                                0
                                                                                                                                                                                                                              Score 82.8; DB 12
Pred. No. 6.8e-09;
                                                                                                                                                                                                                                                                       581
                                                                                                                                                                                                                  Mismatches
                                                                                                                           711
                                                                                                                                                                                                                                                                         G;
                                                                                                                                                                                                                                                                         712 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                          Length 2677
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Query Match

Local

Similarity

10.3%; 97.7%; ₽,

Score 82.8; D Pred. No. 6.8e 0; Mismatches

.8e-09; DB 14;

Length 2677; Indels

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Gape

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712 T; 0 U; 1 Other;

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CC in brain disorders and chosen from any one of 138 nucleotide sequences of throughput method for detecting differential expression of one or more CDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II) celebrated from AEAA3912, AEAA3810, AEAA3810, AEAA3813, AEAA3855, AEAA3856, CE AEAA3883 and AEAA3812, AEAA3813, AEAA3830, AEAA3831, AEAA3855, AEAA3856, CE (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful CC (IV); and (6) a protein (V) produced using CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful CC compounds to identify a ligand which specifically binds a cDNA, where the method involves combining (I) with the library of molecules or compound CC under conditions to allow specific binding and detecting specific binding cC (V), where the protein and recovering the protein from the CC compound. (V) is useful for high throughput method for screening a library of molecules or compound under conditions to allow specific binding which specifically binds (CV), where the method involves combining (V) or its portion with the compound. (V) is useful for purifying a ligand which specific binding to compound under conditions to allow specific binding specific binding between (V) and a molecule or compound. (V) is useful for purifying a ligand from a sample, which the specific binding, recovering the bound protein and separating the convolves immunizing an animal with (V) or its portion with the sample under conditions to convolves immunizing an animal with (V) or its portion under conditions to convolves immunizing an animal with the sample under conditions to convolve in the convolves in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a composition (I) for the diagnosis, staging, treatment or for the monitoring of treatment of a subject with a brain disorder. (I) comprises several cDNAs that are differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; treatment; brain disease; neuroprotective; cerebrop muscular-gen.; cycostatic; neuroleptic; nootropic; antidepress anticonvulsant; analgesic; antiparkinsonian; ophthalmological; immunotherapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful for diagnosis, staging, treating or monitoring treatment of a subject with a brain disorder, comprises several cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 34; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that are differentially expressed in brain disorders.
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RESULT 15
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                      This invention describes a novel method of identifying a compound that inhibits the processing of amyloid-beta precursor protein in a mammalian cell. The invention also describes; a) an agent for inhibiting amyloid-beta precursor processing consisting of an antisense polynucleotide, a ribozyme or a small interfering RNA (slNA), where the agent comprises a nucleic acid sequence complementary to, or engineered from, a naturally-coccurring polynucleotide sequence encoding the polypeptide comprising the amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical composition comprising the agent for inhibiting amyloid-beta precursor processing or an amyloid-beta precursor processing inhibitor in admixture with a carrier indicator of the processing of amyloid-beta precursor protein e.g. a indicator of the processing of amyloid-beta precursor protein e.g. a indicator in substrate of a kinase comprising AEG09268. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a compound that inhibits amyloid-beta precursor protein processing in a mammalian cell for treating e.g., Alzheimer's diseaße by measuring a compound-polypeptide property related to amyloid-beta peptide
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P-PSDB; AEG09284.
REFSEQ; NM_138980.
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mitogen activated protein-kinase inhibitor; neurological disease;
Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
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24-AUG-2004; 2004US-0603948P.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a

Claim 1; SEQ ID NO 29386; 103pp; English.

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Best Local
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                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, use diagnostics, forensics, gene mapping, identification of \mathfrak n responsible for genetic disorders or other traits and to
                                                                                                                                                                                                                     WPI; 2001-639362/73.
P-PSDB; ABG29395.
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23-AUG-2000; 2000US-00649167.
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Matches 81
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                     Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ
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                                                                                                                                                                                     SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping; gene mapping;
                                                                                                                                                                                        2768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.1%;
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                                                                                                                                                                                  103pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 G; 190
                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apping; gene therapy; forensic,
diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 972;
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RESULT 18
AAS75684/c
ID AAS756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc activity of (II) or to treat disease states involving (II). (II) is cuseful for generating antibodies against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and its binding partners are useful in medical imaging cof sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cc amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this catedotic disorders in the printed specification, but was obtained in clectronic format directly from WIPO at fig.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 81
                                                                                     diagnostics, for responsible for biodiversity.
                                                                                                New isolated polynucleotide and encoded polypeptides, use diagnostics, forensics, gene mapping, identification of managements are traits and to responsible for genetic disorders or other traits and to
                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                             tood
                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS75684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS75684 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 999
                                                                                                                                                      P-PSDB;
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                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                     (HYSE-)
                                                                                                                                                      2001-639362/73
DB; ABG11497.
                                                                                                                                                                                                                                                                                                                                                                                           supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393
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                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping; gene mapping; gene therapy;
upplement; medical imaging; diagnostic; genetic of

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
                                                                                                                                                                                                                     HYSEQ INC.
                                                                                                                                                                                           RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  human diagnostic
                                                             11488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA; 1111
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                                                           103pp;
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Pred.
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                                                         English.
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No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                               mutations
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used

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RESULT 19
AAA59379/c
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JNK3; c-jun N-terminal kinase 3; JNK3alphal isoform; JNK3alpha2 isoform; mitogen-activated kinase; neurodegeneration; apoptosis; neuron; neurodegenerative disease; Alzheimer's; Parkinson's; brain injury; Huntington's disease; aging; acquired immune deficiency syndrome; cerebral anoxia; hypoxia; edema; gene therapy; spinal cord injury; retinal degeneration; ss.
                     WPI; 2000-499230/44.
P-PSDB; AAB07788.
                                                                                                                                                                             20-JAN-1999;
26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding
                                                                                                                                                                                                                                                  19-JAN-2000; 2000WO-FR000104
                                                                                                                                                                                                                                                                                                27-JUL-2000
                                                                                                                                                                                                                                                                                                                                        WO200043524-AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                (AVET ) AVENTIS PHARMA SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                                     Fournier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c-jun N-terminal kinase 3 derivative JNK3deltaNalpha1
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                                                                                                                                                                             99FR-00000586.
99US-0122175P.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
142. .1296
                                                                                                                                                                                                                                                                                                                                                                                     /product= "JNK3deltaNalphal'
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                                                                                     Maury
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Pred. No. 2e-08;
0; Mismatches
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                                                                                     Zhou-Liu
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RESULT 20
ABL88411/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3, which have deletions from the N-terminal region corresponding to positions 1-38 of the JNK3alphal and alpha2 isoforms or a C-terminal deletion from position 139. JNK are mitogen-activated kinases implicated in neurodegeneration and apoptosis of neurons. The derivatives are used to identify specific ligands. These ligands, and JNK3-specific antibodies, are used for prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's, Parkinson's or Huntington's diseases, degeneration associated with aging or acquired immune deficiency syndrome, brain injury, or cerebral anoxia, hypoxia or edema. Vector syndrome, brain injury, or cerebral anoxia, hypoxia or edema. Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containing sequences encoding the derivatives are useful in gene therapy, e.g. of spinal cord injury and retinal degeneration. The present sequence encodes the derivative JNK3deltaNalphal
                                      Claim 1; Fig 34; 213pp; German
                                                                                                                          P-PSDB;
                                                                                                                                       WPI; 2002-257469/30
                                                                                                                                                                                                                          03-AUG-2000; 2000DE-01037759
                                                                                                                                                                                                                                                      03-AUG-2001; 2001WO-EP009011
                                                                                                                                                                                                                                                                                14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                              Pain; analgesic; gene therapy; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL88411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1306 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 44-45; 57pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New derivatives of c-jun N-terminal kinase 3, ligands for treatment of neurodegeneration, h
                                                                              Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific peptides
                                                                                                                                                                                                                                                                                                           WO200212338-A2
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          Pain regulated cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          known isoforms.
                                                                                                                                                                                               (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1279 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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                                                                                                                                                                  C
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                                                                                                                          ABB85006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA; 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCCTTGTAGATAAGTTCTTT 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wetzels I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                   disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 A; 281 C; 301 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.1%;
                                                                                                                                                                   Wnendt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.4; DB :
Pred. No. 2e-08;
                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                   Weihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 T; 0 U; 0 Other;
                                                                                                                                                                   (F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of JNK (c-jun N-terminal ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         have specific
                                                                                                                                                                     Schaefer MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for identifying 
lave specific deletions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1306;
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The invention relates to identifying pain-regulating substances comprises (i) incubating a test substance with a cell (or prepar

preparation

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RESULT 21
AED32365/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analgesic activity. (A) along with nucleic acid (ABL88411-ABL88411) that encode proteins (B, ABB85006-ABB85037) that interact with (A), (B), vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention
The invention relates to a novel differentiation inducing agent of a leukemia cell. The agent comprises an expression activator or functional activator of a promyelocytic leukemia (PML) protein, or an expression inhibitor or functional inhibitor of the PMLK protein (a PML specific
                                                                                                      Differentiation inducing agent of leukemia cell useful as leukemia therapeutic agent, comprises expression activator/functional activa promyelocytic leukemia protein, or expression inhibitor/functional inhibitor of PMLK protein.
                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                Kitabayashi
                                                                                                                                                                                                                                                                                                       29-MAR-2004; 2004JP-00097088.
                                                                                                                                                                                                                                                                                                                                     29-MAR-2004; 2004JP-00097088
                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                  JP2005281183-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-2005
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                                                                                                                                                                                                                                                              (-DOXOI
                                                                                                                                                                                                                                                                            (KOKU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1773 BP; 555 A; 410 C; 388 G; 420 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1343
                                                                                                                                                                                   2005-717904/74.
)B; AED32366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promyelocytic leukemia
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                                                                                                                                                                                                                                                         KOKURITSU GAN CENT SOCHO.

DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAATTCATTA 1284
                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                             IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
92. .1360
                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human promyelocytic leukemia protein kinase"
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Pred. No. 2.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute promyelocytic leukemia; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase encoding gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                          Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1262
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RESULT 22
AAS83445/c
ID AAS834
XX AAS834
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XX Human;
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Best Local
                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes, (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to reparating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, u diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and tresponsible for genetic disorders or other traits.
                                                    involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS83445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human promyelocytic leukemia protein kinase (PMLK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n; chromosome mapping;
supplement; medical in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630
                                                                                                                                                                                                                                                                                                                                                                                                                    1; SEQ ID NO 19249; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG19258
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                             aberrant protein expression or biological activity. The de and polynucleotide sequences have applications in
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2000US-00649167
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98.8%;
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imaging; diagnostic;
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Pred. No. 2.
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o assess
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RESULT 23
AEG09276/c
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 propresent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                             Identifying a compound that inhibits amyloid-beta precursor protein processing in a mammalian cell for treating e.g., Alzheimer's disease by measuring a compound-polypeptide property related to amyloid-beta peptide
                                                                                                                WPI; 2006-231019/24
P-PSDB; AEG09285.
REFSEQ; NM_138981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amyloid-beta precursor protein; pharmaceutical; mitogen activated protein-kinase inhibitor; neurological disease; halzhaimer's disease; depeneration; cognitive disorder; Neuroprotective; Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
                       Example 1; SEQ ID NO 12; 84pp; English
                                                                                                                                                                     Spittaels KF,
                                                                                                                                                                                              (GALA-)
                                                                                                                                                                                                                                    12-MAY-2004; 2004US-0570352P.
24-AUG-2004; 2004US-0603948P.
                                                                                                                                                                                                                                                                          12-MAY-2005; 2005WO-EP052182
                                                                                                                                                                                                                                                                                                     17-NOV-2005
                                                                                                                                                                                                                                                                                                                              WO2005109001-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MAPK10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEG09276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                              GALAPAGOS GENOMICS NV
LAENEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACTTCCTTGTAGATAAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcript variant 4 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 459 A; 499 C; 520 G; 394 T; 0 U;
                                                                                                                                                                     Hoffmann
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       /product= "mitogen-activated protein kinase
transcript variant 4"
                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.1%;
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                                                                                                                                                                     Merchiers
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Pred. No. 2.2e-08;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                      10 (MAPK10),
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This invention describes a novel method of identifying

a compound that

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cc The method involves activation of a biological pathway producing an clindicator of the processing of amyloid-beta precursor protein e.g. a composition protein e.g. a comprising AEG09266 AEG09268. The composition for treating or proveries a label indicating use cft the composition for treating or preventing a condition involving cognitive impairment or a susceptibility to the condition. The agent is cuseful in the manufacture of a medicament for inhibiting the processing of amyloid-beta precursor protein in a subject suffering from or cusceptible to the abnormal processing of the protein, or for treating or preventing a condition involving consecution a condition involving consecution in a subject suffering from or consecution a precursor protein in a subject suffering from or cusceptible to the abnormal processing of the protein, or for treating or preventing a condition involving cognitive impairment or a susceptibility to the condition, preferably, Alzheimer's disease. This sequence encodes that a kinase involved in the up-regulation of amyloid-beta 1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
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Best Local
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                                                                                                                                                                                                                                                                                                                 C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; Alzheimer's disease; Huntington disease; amyotrophic lateral ischemia; trauma; motorneuron disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence encoding the polypeptide comprising the amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical composition comprising the agent for inhibiting amyloid-beta precursor processing or an amyloid-beta precursor processing-inhibiting amount of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell. The invention also describes; a) an agent for inhibiting amylo beta precursor processing consisting of an antisense polynucleotide, ribozyme or a small interfering RNA (siRNA), where the agent comprise
                                                Davis RJ,
                                                                                                                      03-OCT-1997;
                                                                                                                                                         05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                       Seq ID No: 6 of WO9918193
                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2003
21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX37276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX37276 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2155 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibits the processing of amyloid-beta precursor protein in a mammalian cell. The invention also describes; a) an agent for inhibiting amyloid-
              WPI; 1999-287734/27
                                                                                                                                                                                            15-APR-1999.
                                                                                                                                                                                                                            WO9918193-A1
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                  human;
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                                                                                     VIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCCTTGTAGATAAGTTCTTT 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAAGGAGAAGGCTGTCCTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                 Flavell RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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(first ent
                                                                                     MASSACHUSETTS
                                                                                                                      97US-0060995P
                                                                                                                                                         98WO-US020904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2372
                                                   Rakic
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                                                   שי
                                                   Whitmarsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                     Kuan
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                                                   'n
                                                   Yang
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Identification of c-Jun N-terminal kinase 3 modulators

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RESULT 25
AAL48611/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method CC comprises (a) incubating a cell that can express a JNK3 protein, or that CC has JNK3 activity, with a compound under conditions and for a time CC sufficient for the cell to express a JNK3 protein/activity without the compound; (b) incubating a control cell under the same conditions and for the same time without the compound; (c) measuring JNK3 expression/CC activity in the cell in the presence of the compound; (d) comparing the CC compound, where a difference in the level of expression/activity. The CC indicates that the compound modulates JNK3 expression/activity. The CC invention also provides a transgenic non-human mammal having a transgene CC disrupting expression of a JNK3 gene, the transgene being chromosomally CC e.g. antisense nucleic acids, are used to treat disorders involving CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, Parkindon's CC disease or epilepsy. JNK3 sequences under GenBank accession numbers CC U34819, U34820, U07620, L27128, L35236, X12740 and V00727 can be used in CC field.)
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Best Local
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                                       12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                     Human; insulin
ISM; diabetes;
                                                                                                                           12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAL48611 standard;
                                                                                                                                                                       11-JAN-2002;
                                                                                                                                                                                                                                WO200255664-A2
                                                                                                                                                                                                                                                                                                                                Human insulin receptor signaling modifier cDNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0
                                                                                                                 12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630
                                                                                                                                                                                                                                                                                      insulin receptor signaling; insulin receptor signaling labetes; metabolic syndrome; antidiabetic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAAITCATTA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCCTTGTAGATAAGTTCTTT
                                       2001US-0261226P.
2001US-0261303P.
2001US-0261335P.
2001US-0261336P.
2001US-0261336P.
2001US-0261456P.
2001US-0261457P.
2001US-0261458P
2001US-0261459P
2001US-0261461P
                                                                                                                                                                        2002WO-US001048
                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA; 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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Pred. No. 2.3e-08;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2372;
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                                                                                                                                                                                                                                                                                                     modifier;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent dentifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM coding sequence described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2372 BP;
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P-PSDB; AAO18492.
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1415 CTTCCTTGTAGATAAGTTCTTT 1394
                                                                 690
                                                                                                                                                                             630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTTCTGAATTCATTA
                                                                                                                                                                                                                                                                   81;
                                                                                                                                                                                                                                                                                                  Similarity
                                      CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                   CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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2001US-0261531P.
2001US-0261532P.
2001US-0261589P.
2001US-0261590P.
2001US-0261694P.
2001US-0261695P.
2001US-0261697P.
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferguson
                                                                                                                                                                                                                                                                                                                                                                                                   714 A; 548 C; 519 G;
                                                                                                                                                                                                                                                                                               10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             స్ట
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kidd
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                               80.4; DB 6;
No. 2.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                                                                   591 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                              Length 2372;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                   1416
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RESULT 26
ACA56791/c
30-JAN-1998;
                31-DEC-2002.
                                                                              Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma
                                                                                                         Human signalling pathway polynucleotide probe
                                                                                                                             06-JUN-2003
                                                                                                                                              ACA56791;
                                                                                                                                                                 ACA56791 standard;
                                                    iomo sapiens
                                                                       .mmunopathy;
                                                                       AIDS;
                                                                                                                             (first entry)
98US-00016434.
                                                                      asthma; neuropathy;
                                                                                                                                                                 CDNA;
                                                                                                                                                                  2372
                                                                       Alzheimer'
                                                                                 adenocarcinoma; leukaemia;
                                                                                                          SEQ
                                                                                                           Ħ
                                                                       disease; microarray
                                                                                                            ŏ
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1389

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RESULT 27
ADI56587/c
ID ADI565
XX ADI565
XX ADI565
XX ADI565
XX ADI565
XX ADI565
XX Human
XX Human;
XW effect
XW effect
XW effect
XW drug d
XW signal
XW bone m
XW diabet
XW dement
XX
OS Homo &
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a combination which, comprises a number of CC polynucleotide probes comprising a sequence selected from one of the 1490 CC sequences mentioned in the specification. The combination is useful as an CC array element in a microarray for monitoring the expression of a number CC of target polynucleotides. The microarray is particularly useful in the CC diagnosis and treatment of cancer and immunopathology and neuropathology. CC The microarray is useful in diagnostics and treatment regimens, drug CC discovery and development, toxicological and carcinogenicity studies, CC forensics and pharmacogenomics. The microarray is also useful for CC monitoring progression of diseases and for developing sophisticated. CC profiles for the effects of currently available therapeutic drugs. The CC combination is also useful for purifying a subpopulation of mRNAs, CDNAs and genomic fragments and in research and diagnostic applications. The CC cardy can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose CC various diseases including cancer e.g. adenocarcinoma and leukaemia, CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and parkinson's disease. The present sequence atta for this patent did not form part of the invention. Note: The sequence atta for this patent did not format directly from USPTO at the printed specification but was obtained in electronic combinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 81
                                                          drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropat dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                             Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector like polypeptide; cancer; immunopathology; neuropathology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2372
                       Homo sapiens
                                                                                                                                                                                                                          Human polynucleotide probe #1389
                                                                                                                                                                                                                                                                    22-APR-2004
                                                                                                                                                                                                                                                                                                          ADI56587
                                                                                                                                                                                                                                                                                                                                                  ADI56587 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAAITCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCCTTGTAGATAAGTTCTTT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1389; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seilhamer JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 714 A; 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00016434.
                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.1%;
                                                                                                                                                                                                                                                                                                                                                  2372
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                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTCTTCTGAATTCATTA
                                                                               neuropathology;
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ADP45599; 26-AUG-2004

(first entry

Human MAP

kinase MAPK10 (JNK3)

CDNA

breast cancer; cytostatic; gene therapy; human; ss; single nucleotide polymorphism; MAP kinase; MAPK10;

gene;

SNP; JNK3A; p493F12; RESULT 28

ADP45599 standard; cDNA; 2372 BP

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                                                                                                                                                                                                                                                 CC comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes CC comprising at least a portion of a gene encoding at transducing CC polypeptide and third polynucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the CC composition are useful as array elements in a microarray for monitoring CC characteristic polynucleotides. The microarray for monitoring CC diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, CC neuropathology. It can also be used for drug discovery and development, CC microarray can also be used for monitoring the progression of diseases CC Microarray be associated with the altered expression of signalling pathway CC polypeptides. The composition can also be used to purify a subpopulation CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone marrow, brain, breast or cervix, CC unicroarray for a neuropathology, e.g. Alzheimer's disease or depression. This sequence data for this patent did not form part of the printed specification but was contained in electronic format directly from USPTO at
                                                                                                                                   Matches
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
                                                                                                                                                                                                      Sequence 2372 BP;
                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; SEQ ID NO 1389; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-090520/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2002; 2002US-00305720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-2004
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                                                                                                                                                     Local
1415
                                                                                  81;
                                                                                                                                                     Similarity
                                                                CTTCCTTGTAGATAAGTTCTTT 1394
                              CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00016434
                                                                                                                                                                                                    714 A; 548 C; 519
                                                                                                                                                  10.1%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a composition of polynucleotide probes
                                                                                                                                     0;
                                                                                                                                                     Score 80.4;
Pred. No. 2.
                                                                                                                                     Mismatches
                                                                                                                                                                                                      <u>ဂ</u>
                                                                                                                                                                                                      591 T; 0 U; 0 Other;
                                                                                                                                                     .3e-08
                                                                                                                                                                     DB 12;
                                                                                                                                     ۲,
                                                                                                                                                                    Length 2372;
                                                                                                                                     Indels
                                                                                                                                     0;
                                                                                                                                     Gaps
                                                                    . 1416
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RESULT 29
ADS92938/c
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                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for identifying a subject at risk of breast cancer comprising detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The method of the invention has cytostatic applications and may be useful for identifying a subject at risk of breast cancer, for early diagnosis, prevention and treatment of breast cancer, possibly via gene therapy, as well as to analyse and predict a response to a breast cancer treatment and in clinical drug trials. The current sequence is that of the human MAP kinase MAPK10 (NWA3, NWA3, p493F12, p54bSAPK MAP kinase; c-Jun kinase 3;NWA3 alpha protein kinase; c-Jun N-terminal kinase 3; stress activated protein kinase beta) cDNA of the
 cytostatic; gene therapy; human;
                    Mitogen-activated protein kinase
                                           02-DEC-2004
                                                                 ADS92938
                                                                                                                                                                                                                                                                            Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
                                                                                    ADS92938 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a subject at risk of breast cancer by detecting the presence of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUMA1 or GALE regions which are associated with breast cancer in a nucleic acid sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roth
                                                                                                                                                                                                                                                                                                 invention which has been mapped to chromosomal position 4q22.1-q23.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-2002; 2002US-0429136P
24-JUL-2003; 2003US-0490234P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-2003; 2003WO-US037948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 4q22.1-q23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p54bSAPK MAP kinase; c-Jun
c-Jun N-terminal kinase 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SEQU-) SEQUENOM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004047623-A2
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                                                                                                                                                                                      1475
                                                                                                                                                                 690
                                                                                                                                                                                                            630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a subject.
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                                                                                                                                                                                                                                  118
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                        CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                     CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                                                                                                                    CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTCATTA
                                                                                                                                            CTTCCTTGTAGATAAGTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nelson MR,
                                                                                                                                                                                                                                  Conservative
                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
224. .1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human MAP kinase MAPK10 (JNK3) protein"
                                                                                      CDNA;
                                           entry)
                                                                                                                                                                                                                                          10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braun
                                                                                                                                                                                                                                                                                                                                                                                                                                            289pp; English.
                                                                                 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase 3; JNK3 alpha protein kinase; stress activated protein kinase beta
                                                                                                                                                                                                                                0
                                                                                                                                                                                                                               Score 80.4; D
Pred. No. 2.3e
0; Mismatches
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                                                                                                                                            1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kammerer
                     10
                                                                                                                                                                                                                                           .3e-08;
                                                                                                                                                                                                                                                     DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reneland
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                     2372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta;
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                                                                                                                                                                                                                                                                                      SNP detection; breast tumor; endocrine disease;
gynecology and obstetrics; neoplasm; cytostatic; metastasis;
                              Human mitogen-activated protein kinase 10 (MAPK10)
                                                                           ADX98578
                                                                                                ADX98578 standard; cDNA; 2372
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(first

entry)

CDNA

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Query Match
Best Local
                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                The invention describes a method of identifying a candidate branching morphogenesis modulating (MBM) agent. The method comprises; providing an assay system comprising a MBM polypeptide or nucleic acid; contacting the assay system with a test agent under conditions where the system provides a reference activity, except for the presence of the test agent; and detecting a test agent-blased activity of the assay system, where a difference between the test agent-blased activity and the reference activity identifies the test agent as a candidate branching morphogenesis in a mammalian cell; and a method of modulating branching morphogenesis in a mammalian cell; and a method for diagnosing a disease in a patient. The method is useful in identifying a candidate branching morphogenesis modulating agent for preparing a composition for diagnosing or treating cancer. This sequence encodes a human branching morphogenesis
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a candidate branching morphogenesis modulating agent treating cancer comprises contacting the assay system comprising polypeptide or nucleic acid with a test agent and detecting a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plowman GD, Karim FD, Swimmer C,
Schulte-Merker S, Langheinrich U,
Odenthal JH, Scheel JK, Will TT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2002;
30-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2003; 2003WO-US033549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        branching morphogenesis modulating agent; MBM agent; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EXEL-) EXELIXIS INC.
1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-365506/34.
                                          690
                                                                                                                                                                              81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity.
                                                                                                                                                                                                     Similarity
                                                                                    CTTCCTTGTAGATAAGTTCTTT 1394
                                                                                                                               CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                        CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                     2372 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 9; 179pp; English
                                                                                                                                                                                                                                                                                                                       (MBM)
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-0420554P
2002US-0436941P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lickteig
                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                     714 A; 547
                                                                                                                                                                                                   10.1%;
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                                                                                                                                                                              0
                                                                                                                                                                                                   Score 80.4;
Pred. No. 2.
                                                                                                                                                                                                                                                                       C; 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mer C, Habeck HA, Kobliz ich U, Stott GM, Trowe T ll TT, Jin Y, Bjerke LM, Hammonds RGR, Amundsen C
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                       <u>ი</u>
                                                                                                                                                                                                                                                                          590 T; 0 U; 0 Other;
                                                                                                                                                                                                   3e-08;
                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                              ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koblizek
                                                                                                                                                                                                                      Length 2372;
                                                                                                                                                                                Indels
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Наі
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.
                                                                                                                                                                              0
                                                                                                                                                                              Gaps
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                                                                                         1416
                                                                                                                                      689
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RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention demonstrates cytostatic activity and may be useful for identifying a risk of, preventing and/or treating breast cancer and cancer metastasis. The methods may be utilized for gene therapy or RNA interference. The current sequence is that of the human mitogen-activated protein kinase 10 (MAPKIO) cDNA of the invention which is located at
                                                          amyloid-beta precursor protein; pharmaceutical; mitogen activated protein-kinase inhibitor; neurological disease; Alzhaimer's disease; degeneration; cognitive disorder; Neuroprote Nootropic; substrate; mitogen-activated protein kinase 10; MAPK10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2003; 2003US-0490234P.
25-NOV-2003; 2003US-00723681.
25-NOV-2003; 2003US-0525239P.
                                                                                                                                                                                                    AEG09273 standard; DNA; 2372
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for identifying a subject at risk of breast cancer comprising detecting the presence or absence of a polymorphic variation associated with breast cancer. The method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; RNA interference; chromosome 4; ss; gene;
mitogen-activated protein kinase 10; Jun N terminal kinase-3; MAPK10
                       Homo sapiens
                                                                                                                            Human MAPK10,
                                                                                                                                                   20-APR-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoyal-Wrightson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roth RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAY-2004; 2004WO-US016939
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                                                                                                                                                                                                                                                                   1415
                                                                                                                                                                                                                                                                                                                   1475
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                                                                                                                                                                                                                                                                                          690
                                                                                                                                                                                                                                                                                                                                            630
                                                                                                                                                                                                                                                                                                                                                                   81;
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     2372
                                                                                                                                                                                                                                                                                                                                            CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                                                                                                                                                                                                       CTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nelson MR,
phtson CR;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                        transcript variant 1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 714 A;
                                                                                                                                                                                                                                                                                                                                                                                10.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617pp; English
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                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                Score 80.4;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                           Length 2372;
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                                                                                                                                                                                                                                                                                                                                                                                                                     0 Other;
                                                              Neuroprotective;
10; MAPK10; ds;
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Key

Location/Qualifiers

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RESULT

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                                                                                                                                                                                                            This invention describes a novel method of identifying a compound that coinhibits the processing of amyloid-beta precursor protein in a mammalian cell. The invention also describes; a) an agent for inhibiting amyloid-beta precursor processing consisting of an antisense polynucleotide, a concurring polynucleotide processing of an antisense polynucleotide, a concurring polynucleotide sequence encoding the polypeptide comprises a composition comprising the agent for inhibiting amyloid-beta mino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical composition comprising the agent for inhibiting amyloid-beta precursor processing or an amyloid-beta precursor processing-inhibiting amount of a mitogen activated protein-kinase inhibitor in admixture with a carrier. The method involves activation of a biological pathway producing an composition for the expression of a reporter e.g. alkaline phosphatase. Composition further comprising AEG09266-AEG09268. The pharmaceutical composition further comprises a label indicating use of the composition for treating or preventing a condition. The agent is consecutive impairment or a susceptibility to the condition. The agent is cusceptible to the abnormal processing of the protein, or for treating or preventing a condition involving of amyloid-beta precursor protein in a subject suffering from or cusceptible to the abnormal processing of the protein, or for treating or preventing a condition preferably, Alzheimer's disease. This sequence encodes chuman mitogen-activated protein kinase 10 (MAPKIO), transcript variant 1, a kinase involved in the up-regulation of amyloid-beta 1-42.
                                                                                                                                      Query Match
Best Local S
Matches 81
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a compound that inhibits amyloid-beta precursor protein processing in a mammalian cell for treating e.g., Alzheimer's disease by measuring a compound-polypeptide property related to amyloid-beta peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-2004; 2004US-0570352P
24-AUG-2004; 2004US-0603948P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFSEQ; NM_002753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spittaels KF, Hoffmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-2005;
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1415
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DB; AEG09282.
                                     690
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                                                                                                                                                          Similarity
                                                                                                                                                                                                            2372
     CTTCCTTGTAGATAAGTTCTTT
                          CTTCCTTGTAGATAAGTTCTGT 711
                                                                      CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                          CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2005WO-EP052182
                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "mitogen-activated protein kinase
transcript variant 1"
                                                                                                                                                                                                          714 A;
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                                                                                                                                                      10.1%;
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Pred.
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       1394
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                                                                                                                                          Mismatches
                                                                                                                                                        80.4;
No. 2
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                                                                                                                                                                                                            590 T; 0 U; 0 Other;
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                                                                                                                                                                          DB
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ACC46216;

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ACC46216;

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ACC46216;

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O2-JUN-2003 (first (
DX

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Human dithp intracel)

XX

Human; dithp; diagnowed (
Cancer; cell prolife;

KW

Inflammatory disorde

KW

Inflammatory disorde

KW

Inflammatory disorde

KW

Intracellular signal

CS

Homo sapiens.

XX

PH

O5-DEC-2002; 2002WO-

XX

PF

28-MAR-2001; 2001US-

PR

29-MAR-2001; 2001US-

PR

29-MAR-2001; 2001US-

PR

29-MAR-2001; 2001US-

PR

29-MAR-2001; 2001US-

PR

17-MAY-2001; 2001US-

PR

                                                                                                             The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHF) ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA comparisons comprising a dithp nucleic acid sequence; the transgenic organisms comprising a dithp nucleic acid sequence; the crecombinant production of DITHF proteins; antibodies specific for DITHF proteins; microarrays comprising a dithp nucleic acid sequences; methods of contents of dithp nucleic and sequences; methods of contents of the toxicity of test compounds using a dithp hybridiation of assessing the toxicity of test compounds using a dithp hybridiation cropose. Dithp nucleic acid sequences and DITHF proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, curval, fungal or parasitic infections; hormonal disorders; metabolic disorders; and connective tissue disorders. They may also be used to be of the conditions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dufour GE, Hillman JL, Yu JY, Tuason O, Daughtery SC, Dam TC, Liu TF, Nguyen DA, Peralta CH, David MH, Lewis SA, Chen AJ, Flores V, Marwaha R, Lo A, Lan RY, Urash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; antisense therapy; genot disease model; toxicological testing; intracellular signalling; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human dithp intracellular signalling protein-encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; SEQ ID NO 137; 591pp; English.
        for modulators of protein activity or gene expression. DITHP ns can additionally be used in analysis of the proteome of a 1 type and to induce antibodies. The dithp nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0280068P.
2001US-0291280P.
2001US-0291849P.
2001US-0299428P.
2001US-0299476P.
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2001US-0280067P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gietzen D, C
O, Yap PE, A
DA, Kleefeld
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Yap PE, Amshey SR;
Kleefeld Y, Gerstir
Panzer SR, Harris E
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RESULT 33
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                   The invention relates to a new composition comprising ADI61633-ADI61770 and their complements that are cDNAs differentially expressed in brain disorders. Also included are a high throughput method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids and a high throughput method for screening a library of molecules or compounds to identify a ligand that specifically binds a cDNA. The expression of the each of the cDNAs is downregulated at least two-fold in the brain of the subjects with Alzheimer's disease (ADI61727) or upregulated at least two fold in Alzheimer's disease (ADI61728-ADI61770). The composition is useful for diagnosing or treating Alzheimer's disease. The present sequence is a cDNA downregulated at least two-fold in the brain of the subjects with Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence representes a dithp cDNA encoding a DITHP protein which has intracellular signalling activity. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 33; 223pp; English.
                                                                                                                                                                                                                                                                       New composition comprising cDNAs that are differentially expressed brain disorders, useful for diagnosing or treating Alzheimer's disc
                                                                                                                                                                                                                                                                                                                            WPI; 2004-118572/12
                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-2000; 2000US-00566921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-2000; 2000US-00566921
                                                                                                                                                                                                                                                                                                                                                           Loring JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ss; Alzheimer's disease; differential display; neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2945 BP; 878 A; 637 C; 671 G; 759 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             additionally useful in somatic or germline gene therapy
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              two-fold
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          brain of
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Pred. No. 2
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            the subjects
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treatment or for the monitoring of treatment of a subject with a brain disorder. (I) comprises several cDNAs that are differentially expressed in brain disorders and chosen from any one of 138 nucleotide sequences of AEA43798-AEA43935, or their complements. Also described: (1) a high Ct throughput method for detecting differential expression of one or more CDNAs in a sample containing nucleic acids; (2) an isolated CDNA (II) containing nucleic acids; (2) an isolated CDNA (II) containing (III); (5) a protein (V) produced using (IV) and (6) a pharmaceutical composition comprising (V). (I) is useful Cf or a high throughput method of screening a library of molecules or compounds to identify a ligand which specifically binds a CDNA, where the method involves combining (II) with the library of molecules or compound to identify a nolecule or compound to a contain, which involves culturing (IV) under conditions to allow specific binding and detecting specific binding the expression of the protein and recovering the protein from the culture. (V) is useful for bigh throughput method for screening a library of molecules or compounds to identify a ligand which specifically binds or conditions for the expression of the protein and recovering the protein from the CC culture. (V) is useful for high throughput method for screening a library of molecules or compounds to identify a ligand which specifically binds (V), where the method involves combining (V) or its portion with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful for diagnosis, staging, treating or monitoring treatment of a subject with a brain disorder, comprises several cDNAs that are differentially expressed in brain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 33; 231pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscular-gen.; cytostatic; neuroleptic; nootropic; antidepressant;
anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA differentially expressed in
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                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a composition (I) for the diagnosis, staging,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loring
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Pred. No. 2.4e-08;
0; Mismatches 1
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ARBSULT 35
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Best Local S
Matches 81
The invention relates to a polynucleotide (I) comprising: (a) a regulatable promoter; (b) a test gene; (c) an IRES sequence; and (d) a surface marker coding sequence comprising a secretion signal sequence, a detectable label protein and a membrane protein where expression of the test gene also results in expression of the surface marker. A method is provided for identifying a host cell that exhibits regulated expression of a test gene complex that comprises (a) providing more than one host cell; (b) inducing the promoter; and (c) selecting a host cell that displays the surface marker on its surface. (I), the host cell and the method are useful for the rapid isolation of candidate eukaryotic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library of molecules or compound under conditions to allow specific binding and detecting specific binding between (V) and a molecule or compound. (V) is useful for purifying a ligand from a sample, which involves combining (V) or its portion with the sample under conditions to allow specific binding, recovering the bound protein and separating the protein from ligand. (V) is also useful for producing an antibody, which involves immunizing an annimal with (V) or its portion under conditions to elicit an antibody response, isolating animal antibodies and screening the isolated antibodies with the protein. (II) is useful in gene therapy for the treatment or prevention of conditions and disorders associated with immune response. The present sequence represents a human cDNA sequence which is differentially expressed in brain tissues, which is useful in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide for rapid isolation of candidate eukaryotic cell clones comprises a promoter, a test gene, an IRES sequence and a surface marker.
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label protein;
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Pred. No. 2.4e-08;
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RESULT 36
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                         Query Match
Best Local (
                                                                                                                            A cDNA clone (AAT10640) was obtd. that codes for rat proline-directed stress-activated protein kinase (SAPK) p54 beta-I (AAR89410). This cDNA, and others (see AAT10638-39 and AAT10641-42) coding for p54 alpha-I, alpha-II, beta-II and gamma (AAR89408-9 and AAR89411-12), were isolated from a rat brain cDNA library following PCR amplification using primers based on p54 tryptic peptides obt. from a cycloheximide-treated rat
                                                                                                                                                                                                                                                                                                                                                            DNA encoding recombinant P54 stress activated protein kinase related antibodies, useful for treating inflammation, hypoxia
                                                                                                                                                                                                                                                                                          Claim 20; Page 44-45; 68pp; English
                                                                                                                                                                                                                                                                                                                                            stress, and
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-106355/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stress activated protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation;
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ONTARIO CANCER INST
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                         BP; 556 A; 506 C; 488 G; 425 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avruch J,
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364. .1644
/*tag= a
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                     86.0%;
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                         Score 66.8;
Pred. No. 2.
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Pred. No. 3e-08;
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  les 12;
                                            DB 2;
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                                        Length 1975;
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Matches 74
                                                                                                                                                                            The invention relates to identifying pain-regulating substances (A) comprises (i) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analyssic activity. (A) along with nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention
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and
                                                                                                                                                       Sequence 1975 BP;
                                                                                                                                                                                                                                                                                                                                                                                                            Identifying pain-regulating compand for diagnosis, by measuring
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1445 ATTACTTCCTTGTAGATGAGTTCTTT 1420
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               ATTACTTCCTTGTAGATAAGTTCTGT
                                                    GCACCTGAAGGTGAGGGCTGGCCTTTGACTACGCCGTTCTTAGTCTTCTCTTCTGAGTTC
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Pred. No. 2.8e
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                                                                                                                                                       425 T;
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                                                                                               AAT10641
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1240 BP; 359
                   26-APR-1996
                                                         AAT10641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying pain-regulating compounds, useful for treating chronic pain and for diagnosis, by measuring binding of compounds to specific peptides
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nes 72; Conserv
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                                                                                                 standard;
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ilarity 87.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             G.
                                                                                                                                                                                                                                                                                                                                                    265 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0 U;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 1240;
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26-APR-1996 AAT10642;

(first entry)

AAT10642 standard;

CDNA; 1408

Stress activated

protein kinase

p54 gamma cDNA.

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RESULT 40
AAT10642/c
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Best Local
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                                                                                                                                                                                                                                                                                                 A cDNA clone (AAT10641) was obtd. that codes for rat proline-directed stress-activated protein kinase (SAPK) p54 beca-II (AAR89411). This cl and others (see AAT10638-40 and AAT10642) coding for p54 alpha-I, alph II, beta-I and gamma (AAR89408-10 and AAR89412), were isolated from a brain cDNA library following PCR amplification using primers based on tryptic peptides obt. from a cycloheximide-treated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding recombinant P54 stress activated protein kinase related antibodies, useful for treating inflammation, hypoxia stress, and for drug screening.
                                                                                                                                                                                                                                                                Sequence 1986 BP; 559 A; 510 C; 488 G; 427 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stress activated protein kinase; SAPK; p54 inflammation; hypoxia; heat stress; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kyriakis JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP
(ONTA-) ONTARIO CANCER IN
                                                                   1447
                                                                                                                                   1507
                                                                                                                                                          630 CTGAAGGAAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                   Similarity
                                                                     CTTCCTTGTAGATGAGTTCTTT 1426
                                                                                                  CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                   CTGAAGGTGAGGGCTTGGCCTTTGACTACGCCGTTCTTAGTCTTCTCTTCTGAGTTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                    Page 46-47; 68pp; English
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avruch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00240014.
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1549
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/note= "base 1549 is
probably C or G"
1550
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/note= "base 1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase
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                                                                                                                                                                                                  Score 64.4; Di
Pred. No. 9.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woodgett
                                                                                                                                                                                                                       .7e-05
                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                   Length 1986;
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alpha-
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                                                                                                                                       1448
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RESULT 41
ABT09489/c
ID ABT094
XX ABT094
XX ABT094
XX O5-DEC
XX Phase-
XX Phase-
XX Rat; t
KW drug d
XX Ratus
XX Ratus
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Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                     A GUNA GIONE (AAT10642) was obtd. that codes for rat proline-directed stress-activated protein kinase (SAPK) p54 gamma (AAR89412). This cDNA, and others (see AAT10638-41) coding for p54 alpha-I, alpha-II, beta-I at beta-II (AAR89408-I1), were isolated from a rat brain cDNA library following PCR amplification using primers based on p54 tryptic peptides obt. from a cycloheximide-treated rat
  29-JAN-2002; 2002WO-US002935.
                       29-AUG-2002
                                             WO200266682-A2
                                                                                        Rat; toxicity study; rat toxic response gene; drug development; phase-1 rat CT gene; ds.
                                                                                                                          Phase-1
                                                                                                                                                05-DEC-2002
                                                                                                                                                                                           ABT09489 standard;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1408 BP; 408 A; 310 C; 339 G; 351 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-106355/12
P-PSDB; AAR89412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEHO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stress activated protein kinase; SAPK; p54 gamma; antibody; inflammation; hypoxia; heat stress; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-1995;
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                                                                                                                                                                                                                                                                                              1317
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                                                                                      development;
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                                                                                                                                                                                                                                                                                                                    626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Page 47-48; 68pp; English.
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                                                                                                                          Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oding recombinant P54 stress activated protein kinase - antibodies, useful for treating inflammation, hypoxia
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ONTARIO CANCE
                                                                                                                                                                                                                                                                 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                   GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                              GCACCTAAAGGAGACGGCTGCCCTCTTATGACGCCATTCTTAGTTCGCTCCTCCAAATCC
                                                                                                                                                                                                                                                 ATGACCTCCTTGTATATCAGTTCTTT 1232
                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                         6.3%;
ilarity 74.4%;
Conservative
                                                                                                                                               (first
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                                                                                                                       gene
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176. .1408
/*tag= a
                                                                                      phase-1
                                                                                                                                                                                          DNA;
                                                                                                                          SEQ ID
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Pred. No. 0.
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                                                                                                   toxicological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JR,
                                                                                                                                                                                                                                                                                                                                                             Length 1408;
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                                                                                                                                                                                                                                                                                              1258
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RESULT 42
ADG30924/c
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Best Local S
Matches 62
Predicting the liver toxicity of an agent to an individual by using test expression profile with a set of reference expression profiles Predictive Model to determine whether the agent will reduce liver toxicity in the individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method used for evaluating the toxicity of an agent comprising determining the expression of a rat toxic response gene(s) in the test animal in response to the agent. The method is useful in drug development, particularly for conducting toxicity studies and analysis before a new drug or compound is approved for human consumption or use. The method is also useful in determining toxicological responses to a new drug. This polynucleotide sequence represents a phase-1 rat CT gene of the invention
                                                                                Kier L,
                                                                                                                              01-APR-2002;
                                                                                                                                                     01-APR-2003; 2003WO-US010141
                                                                                                                                                                                                   WO2003085083-A2
                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                 liver toxicity;
                                                                                                                                                                                                                                                                       Liver toxicity
                                                                                                                                                                                                                                                                                                 26-FEB-2004
                                                                                                                                                                                                                                                                                                                         ADG30924;
                                                                                                                                                                                                                                                                                                                                                ADG30924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evaluating the toxicity of an agent, useful in drug development or in determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in
                                                                                                         (PHAS-)
                                                                                                                                                                             16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 247; 388pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2001;
26-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
62; Conserv
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                                                                                                         PHASE 1 MOLECULAR TOXICOLOGY.
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                                                                                 Nolan
                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                          ACTICCITGIAGATAAGITCIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTAAAGGAGACGCCTGCCCTTATGACGCCATTCTTAGTTCGCTCCTCCAAATCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATT 688
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                                                                                                                                                                                                                                                                                                                                                                                                          ACCTCCTTGTATATCAGTTCTTT
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ilarity 74.7%;
Conservative
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                                                                                                                               2002US-0369287P
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2001US-0308161P
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                                                                                                                                                                                                                                                                        predictive DNA 104.
                                                                                                                                                                                                                                                  Norway rat;
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                                                                                 Sankar U,
                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                  24 hour
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49.4;
Pred. No. 0
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                                                                                 Derbel
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                                                                                                                                                                                                                                                                                                                                                                                                          412
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                                                                                                                                                                                                                                                   combo All;
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Claim

<u>ب</u>

Page 168; 379pp; English

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RESULT 43
ADG45512/c
ID ADG455
XX ADG455
XX ADG455
XX Iiver
XX Iiver
XX Iiver
XX Iiver
XX Iiver
XX Rattus
XX W02003
XX W02003
XX W02003
XX W02003
XX W1-MAY
XX IO-MAY

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Best Local
The present invention describes a method for predicting the liver toxicity in an individual to an agent. The method comprises: (a) obtaining a biological sample from the individual treated with the age (b) measuring the expression of one or more liver toxicity predictive genes in the sample; and (c) using the test expression profile with a of reference expression profiles in a Predictive Model to determine whether the agent will induce liver toxicity in the individual. Also described: (1) predicting the liver toxicity in a agent using an in vitro system; (2) predicting the liver toxicity in a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for predicting the liver toxicity of an agent to an individual comprising obtaining a biological sample from an individual treated with the agent, measuring the expression of one or more liver toxicity predictive genes in the sample and using the test expression profile with a set of reference expression profiles in a predictive model to determine whether the agent will reduce liver toxicity in the individual. The method of the invention may be useful for predicting the liver toxicity of an agent to an individual. The current sequence is that of the liver toxicity predictive DNA of the invention which represents a 24 hour combo All gene.
                                                                                                                                                                                                                                                                                                                                                                   Predicting the liver toxicity in an individual to an agent by
the expression of one or more liver toxicity predictive genes
sample from the individual treated with the agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2003; 2003WO-US014832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-042456/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2002; 2002US-0379831P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liver inflammatory predictive gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629
                                                                                                                                                                                                                                                                                                        7; Fig 4; 336pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; liver toxicity; liver toxicity predictive gene; inflammation predictive gene; inflammation; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHASE-1 MOLECULAR TOXICOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nolan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 BP; 170 A; 129 C; 145 G; 125 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTAAAGGAGACGGCTGCCCTCTTATGACGCCATTCTTAGTTCGCTCCTCCAAATCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%;
74.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΒP
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Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derbel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                               measuring in the
                                                                                                                                                                                    the agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                   set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435
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Query Match
Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                              programmable machine; (3) a computer program product for enabling a computer to perform Predictive Model analysis for liver toxicity on a biological sample from an individual, in vitro cell cultures or explants to an agent; (4) a computer system adopted to predict liver toxicity in a biological system from an individual, in vitro cell cultures or explants to an agent; (5) a computer program product for predicting liver toxicity from a test sample expression profile; (6) mining genes predictive of liver toxicity; (7) an integrated system for predicting liver toxicity; and (8) identifying one or more liver inflammation predictive genes. The method is useful for predicting the liver toxicity in an individual to an agent: The presents aguence that represents a 24 hour combo 3 gene, which is specifically claimed in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                      Sequence 580
434
                                                                                                    494
                                                                                                                                                                                                                            Similarity
                                  ACTTCCTTGTAGATAAGTTCTGT
ACCTCCTTGTATATCAGTTCTTT 412
                                                                                                  ccranaggagacggcrigcccrcrrargacgccarrcrragrregerecrccrccanarccarg
                                                                                                                                                 CCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATT
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                      B₽;
                                                                                                                                                                                                                                                                                                   170 A; 129 C; 145
                                                                                                                                                                                                                            6.2%;
                                                                                                                                                                                              Score 49.4; DI
Pred. No. 0.19
0; Mismatches
                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                                                      <u>ن</u>
                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                            .19;
                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                   T; 0 U;
                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                      11 Other;
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                                                                                                                                                                                                      0
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RESULT 44
ADR91158/c
ID ADR911
XX ADR911
XX Spleer
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OS Unider
XX W02000
AX OF 17-MAI
XX WFI;
XX Claim
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CC Splee
CC Tor p
                                                                                                                                                                              17-MAR-2004; 2004WO-US008371
                                                                                                                                                                                                                                         altered
                                                                                                                                                                                                                                                        Spleen necrosis predictive
                                                                                                                                                                                                                                                                                     ADR91158;
                                                                                                                                                                                                                                                                                                   ADR91158 standard;
                                                                                                                                                                                                             WO2004083402-A2
                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                      16-DEC-2004
                                                                                                                                                                                                                                        expression; toxic response;
                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                   CDNA;
                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                   580
                                                                                                                                                                                                                                                        cDNA sequence,
                                                                                                                                                                                                                                         spleen;
                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                          toxicity; lymphoid;
                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                        114.
                                                                                                                                                                                                                                          gene;
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88

detecting the altered expression of genes in a toxic response of the spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348) or their complete complements. The invention further comprises: monitoring the treatment of compound toxicity in a sample; predicting the spleen toxicity in an individual to an agent; predicting the spleen toxicity of an agent using an in vitro system; a computer program product for predicting spleen toxicity from an expression profile of nucleic

responses species.

Claim 1;

SEQ

ij

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114;

249pp;

English.

New composition comprises cDNAs useful for detecting altered expression of genes in a toxic response of the spleen or for predicting toxic responses to one or more agents including lymphoid tissue types or other

17-MAR-2003; 2003US-0455443P

(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC

2004-691048/67

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Kier L,

Derbel M,

Nolan T;

В Ś 망 ş

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RESULT 45
ADB33776/C
ID ADB33
XX ADB3
XX ADB3
XX ADB3
XX ADB3
XX Human
XX Human
XX Human
XX Homo
XX Signa
XX Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc acids from a sample under test, comprising a computer readable medium cc bearing an encrypted training data set, encrypted lists of genes selected cc from the cDNAs, and a predictive model for causing a general purpose cc computer to predict the spleen toxicity of the sample based upon the cc training data set, the list of genes selected from the cDNAs, and the cc expression profile of nucleic acids from the sample; and an integrated cc system for predicting spleen toxicity, comprising means for measuring cc gene expression profiles of spleen predictive genes from samples exposed ct to the test agent and a computer system operably linked to the means that cc is capable of implementing a predictive model. The composition comprising cc cDNAs is useful for detecting altered expression of genes in a toxic cresponse of the spleen or for predicting toxic responses to one or more capens including lymphoid tissue types or other species. The predictive genes and models of the invention are useful for identifying and cc evaluating various in vitro systems that can be used to accurately predict in vivo toxicity. This polynucleotide sequence represents one of the genes predictive for spleen necrosis of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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signal
  WPI; 2003-450961/43
P-PSDB; ADB65746.
                                                                                                                                                                                                                                                                    05-NOV-2001;
25-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                 28-MAR-2002; 2002EP-00007401
                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1308459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB63776 standard; cDNA; 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                           Yamamoto
                                                                                                                                                                                         (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; pharmaceutical; diagnostic; gene therapy;
regeneration; cell regeneration; membrane protein;
transduction-related protein; transcription-related protein;
orosis; neurological disease; cancer; tumour.
                                                                                                                                                                                      HELIX RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                             J, Isono
Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATT 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTAAAGGAGACGGCTGCCCTCTTATGACGCCATTCTTAGTTCGCTCCTCCAAATCCATG
                                                                                Sugiyama T,
I, Isono Y,
Oshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding
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                                                                                                                                                                                                                                                                    2001JP-00379298
2002US-00350978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 389. .694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Clone UTERU20065470 protein"
                                                                                                                                                                                      INST.
BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone UTERU20065470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 129 C; 145
                                                                                   Otsuka M,
                                                                                                           Hio Y,
                                                                                                                                    Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49.4;
Pred. No. 0.
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                                                                                                           Otsuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                             Wakamatsu A, S
suka K, Nagai K,
Nagahari K, Mas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                     Masuho
                                                                                                                                  Sato H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 Other;
                                                                                                           ø
                                                                                                                                    Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                           Tamechika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435
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New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or targets of gene therapy.

The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide CC of the polynucleotide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide CC of the polynucleotide by contacting the polypeptide or peptide CC peptide of the encoded protein, and observing the binding CC expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe CC proteins are useful as pharmaceutical agents and many disease-related CC genes may be included in them, for developing a diagnostic marker or CC of gene therapy. The genes are involved in tissue and/or cell cc regeneration. Membrane proteins, signal transduction-related proteins, can be used as indicacors for diseases (e.g. osteoporosis, cercoding them can be used as indicacors for diseases (e.g. osteoporosis, cercoding them can be used as indicacors for diseases (e.g. osteoporosis, cercoding them can be used as indicacors for diseases (e.g. osteoporosis, cercoding them can be used as indicacors for diseases (e.g. osteoporosis, cercoding them can be used as indicacors for diseases (e.g. osteoporosis, cercoding them can be used as indicacors for diseases (e.g. osteoporosis, cercoding them can be used as indicacors for diseases. The equilate to the activity or expression of the encoded protein to treat diseases. The sequence proteins and controlled specification, but the sequence of the s

Sequence 2372 BP; 682 A; 440 C; 486 G; 764 T; 0 U; 0 Other;

80

10;

Length

멍 5 맑 S Matches Query Match Best Local Local 1322 989 1 Similarity 65; Conserv ATTACTTCCTTGTAGATAAGTTCTGTAAGAAA GCACCTAAAGGAGAGGGCTGCCCCCGTATAACTCCATTCTTGGTTCTCTCCCCAAGTCC GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC ATAACTTCCTTATATATCAATTCTGTAAAAGA Conservative 6.1%; 70.7%; 0 Score 48.8; Pred. No. 0. Mismatches 717 27; Indels 0 Gape 685 0

RESULT 46 ADJ64020 ADJ64020 standard; DNA; 1765 ₽₽

DNA sequence encoding JNK2 protein.

06-MAY-2004

(first entry)

c-Jun N-terminal kinase; cytostatic; immunosuppressive; dermatological; antiinflammatory; cardiant; antirheumatic; antiarthritic; anti-HIV; respiratory-Gen; antipsoriatic; vasotropic; antibacterial; antilipaemic; cancer; colon cancer; renal cell carcinoma; prostate cancer; non-small cell carcinoma; psoriasis; pemphigus vulgaris; Behcet's syndrome; acute respiratory distress syndrome; ARDS; Behcet's syndrome; post-dialysis syndrome; leukaemia; ischaemic heart disease; post-dialysis syndrome; leukaemia; rheumatoid arthritis; AIDS; vasculitis; septic shock; inflammation; Synthetic lipid histiocytosis; 59. .1333 /product= /\*tag= Location/Qualifiers JNK; "JNK2 protein" ds.

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RESULT 47
AAQ85309/c
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                     as colon cancer, renal cell carcinoma, prostate cancer, and non-small cell carcinoma, and non-malignant or immunological-related cell proliferative diseases, such as psoriasis, pemphigus vulgaris, Behcet's syndrome, acute respiratory discress syndrome (ARDS), ischaemic heart disease, post-dialysis syndrome, leukaemia, rheumatoid arthritis, AIDS, vasculitis, septic shock, and other types of inflammation or lipid histiocytosis. The polypeptide of the invention may be useful in a screening method for identifying molecules which modulate its activity which are potentially useful as therapeutics. The present sequence encoding the JNK2 protein used in the
                                                        AAQ85309
25-MAR-2003
                            AAQ85309;
                                                                                                                                                                                                                                                                                                                 Sequence 1765 BP; 539
                                                                                                                                                                                                                                                                                                                                               exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          terminal kinase (JNK) such as competitive inhibitor peptides, antiboc and sense or antisense polynucleotides which are useful for treating proliferative disorders associated with JNK. These include cancers is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel polynucleotide encoding a c-Jun N-terminal kinase that phosphorylates the c-Jun N-terminal activation domain. The polynucleotide sequence of the invention may have cytostatic, immunosuppressive, dermatological, antiinflammatory, cardiant, antitheumatic, anti-HIV, respiratory-Gen, antipsoriatic, vasotropic, antipacterial, antilipaemic activities Also disclosed in the invention are modulators of the activity or expression of the c-Jun N-terminal antilipaemic activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding a c-Jun N-terminal kinase (JNK), and the encoded polypeptide, useful for (identifying compounds for) treating cancer, psoriasis, rheumatoid arthritis, or septic shock.
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(HIBI/)
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14-DEC-1999
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HIBI M.
LIN A.
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                                                        standard; DNA; 1780
                                                                                                                                                                                                                  CTGAAGGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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(revised)
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98US-00150201.
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94US-00220602.
94US-00276860.
95US-00444393.
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Pred. No. 0.41
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RESULT 48
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Best Local
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immunological disorder; non-malignant cell-proliferative disorder;
leukaemia; organ related malignancy; acute inflammation;
c-Jun N-terminal kinase 2; JNK 2; immunopathological disorder;
                                                                                                                                                                                                                                                                                                                                           Sequence 1780 BP; 541 A; 363 C; 402 G; 474 T; 0 U; 0 Other;
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                                               cDNA encoding
                                                                         20-NOV-2003
                                                                                                                           ADA26313 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 57; Fig 28; 143pp; English
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(UYMA-)
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25-MAR-1994;
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UNIV MASSACHUSETTS MEDICAL SCHOOL
                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                            CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                          CTTCTTTGTAAATTAGCTCTTT 1115
                                                                                                                                                                                                                                           CTGCATCTGAAGGCTGATCTTTACAACACCATTCTTGCTTCTTT
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94US-00220602
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                                                                                                                                                                                                                                                                                                       6.0%;
74.4%;
                                                 N-terminal kinase 2, JNK2
                                                                         entry)
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1137

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CC The invention relates to a method of treating an immunological disorder, con-malignant cell-proliferative disorder, leukaemia, an organ related CC malignancy or acute inflammation, associated with c-Jun N-terminal kinase CC (JNK), comprising administering to a subject, a compound which modulates CC the kinase activity. The method is useful for treating an immunological CC disorder, non-malignant cell-proliferative disorder; leukaemia, an organ CC related malignancy and acute inflammation. The disorder is associated CC with immunological disorder is an immunopathological disorder and is CC respiratory distress syndrome (ARDS), AIDS or rheumatoid arthritis. The CC disorder associated with non-malignant cell-proliferative disorder is CC psoriasis, pemphigus vulgaris, ischaemic heart disease, leukaemia, post CC dialysis disorder and vasculitis. In organ related malignancy, the 'organ CC tisact. The present sequence represents cDNA encoding c-Jun N-terminal CC tract. The present sequence represents cDNA encoding c-Jun N-terminal
                                                                                                                                         Query Match
Best Local S
Matches 61
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13-FEB-1997;
08-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating immunological disorder, non-malignant cell-proliferative disorder, organ related malignancy or acute inflammation, associated co-Jun N-terminal kinase, by giving a compound which modulates kinase
                                                                                                                                                                                                                                   Sequence 1780 BP; 541 A; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Karin M,
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18-JUL-1994;
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HIBI M.
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  CTTCCTTGTAGATAAGTTCTGT
                                            Hibi M,
                                                                                                                                      6.0%;
ilarity 74.4%;
Conservative
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94US-00220602.
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59. .1333
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disease; leukaemia; post dialysis disorder; vasculitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "JNK2"
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                                                                                                                                    Score 48.4; D. Pred. No. 0.41 0; Mismatches
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711
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Best Loc Matches Query Match

61;

Conservative

<u>,,</u>

Mismatches

Local

Similarity

74.4%; 6.0%;

Score 48.4; Pred. No. 0

ВB 9; 21;

Length 1780; Indels

0

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RESULT 49
ACA62801/c
ID ACA62801 standard; DNA; 1780
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18-JUL-1994;
19-MAY-1995;
13-FEB-1997;
08-SEP-1998;
                                                   which is useful for treating a cell proliferative disorder, where the effect is inhibition or stimulation of the kinase, and the composition is an immunosuppressing agent. The composition identified by the above method, is useful for treating a cell proliferative disorder e.g. cancer psoriasis, pemphigus vulgaris, Behcet's syndrome, acute respiratory distress syndrome (ARDS), ischaemic heart disease, leukaemia, rheumatoid
                                                                                                                                      The invention relates to a method of identifying a composition useful treating a proliferative disorder, affecting a kinase having serine an threonine kinase activity and phosphorylating a c-Jun N-terminal activation domain. The method is useful for identifying a composition
                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                       Identifying a composition useful to treat a cell proliferative disorder, comprises incubating the composition and a serine/threonine kinase or polynucleotide encoding the kinase and measuring the effect of the composition on the kinase.
                                                                                                                                                                                                                                                                                                               P-PSDB;
 Sequence 1780
                                          arthritis,
                                                                                                                                                                                                                                                                                                                                                         Karin
                                                                                                                                                                                                                                                                                                                                                                                  (KARI/)
(HIBI/)
(LINA/)
                             represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    threonine kinase; psoriasis; pemphigus vulgaris; Behcet's syndrome; acute respiratory distress syndrome; ARDS; ischaemic heart disease; leukaemia; rheumatoid arthritis; AIDS; vasculitis; septic shock; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-1999;
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                                                                                                                                                                                                             3; Page 32-34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JNK2; cell proliferative disorder; serine kinase; ss; gene; ine kinase; psoriasis; pemphigus vulgaris; Behcet's syndrome; respiratory distress syndrome; ARDS; ischaemic heart disease;
                                                                                                                                                                                                                                                                                                                                                                                  KARIN M.
HIBI M.
LIN A.
                                                                                                                                                                                                                                                                                                                ABU62138
                           AIDS, vasculitis and septic shock. The pthe human c-Jun N-terminal kinase, JNK2,
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  BP;
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94US-00276860.
95US-00444393.
97US-00799913.
98US-00150201.
99US-00461649.
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contained modifications, namely phosphorothioate linkages and 2'methoxyethoxy bases. Some C residues also had a 5'methyl modification. Inhibitors of the TNF alpha signalling molecules have antibacterial, immunosuppressive, antipsoriatic, antidiabetic, antithyroid, cytostatic, dermatological, antiallergic and antiinflammatory activity. The antisense inhibitors may be useful for the treatment of sepsis, rheumatoid arthritis, inflammatory immune disease, inflammatory bowel disease, allergic contact dermatitis, psoriasis, diabetes, Grave's disease, allograft rejection and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel method for modulating cell adhesion molecule expression involves antisense inhibition of a tumour necrosis factor (TWF) alpha signalling molecule. In the method TNF alpha signalling molecules Ha-ras, C-raf and C-Jun N-terminal kinase (JNK) 2 were inhibited by antisense oligonucleotides. In addition an antisense oligonucleotide to the cell adhesion molecule E-selectin was also examined. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                         human JNK2 DNA. This sequence was used to generate the JNK2 antisense oligonucleotide. The antisense oligonucleotide used in the method contained modifications namely should be a second to the method contained modifications namely should be a second to the method contained modifications namely should be a second to the method contained modifications namely should be a second to the method contained modifications namely should be a second to the method contained modifications namely should be a second to the method to the second to the second to the method to the second to the second to the method to the second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating cell adhesion molecule expression for treating immune or inflammatory diseases involves treating cell with specific inhibitor of Tumor Necrosis Factor alpha signaling molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 88-90; 100pp; English.
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Search completed: July 19, Job time : 658 secs

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BM704479 U1-B-CK1-BM50852 iii7a11.y
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CR859197 PONGO PYG
CCF408622 CJ349156
DA807178 DA807178
BFF857793 QV1-FT028
AW314598 10855 MAR
DW91521 J391834 M
BE752836 205445 MAR
DW91521 LB0288 CR
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Email: mdadams@tigr.org
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (Dases 1 to 401)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K. Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ046186 401 bp DNA linear GSS 14-Apr-1999 RPCIII-31H10.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31H10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                               ATGAGGCACATTTACCCCTTTAGCCCATGTTAACATTTTCTTCAGGATTCATTACTATTAA 399
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens (human)
                                                                                                                                                                                                                                               /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                       clone="RPCI-11-31H10"
                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                 49.7%;
                                                                                                                                                                                                                                                                                    type="Lymphocytes"
=_lib="RPCI-11"
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CNS00EO7
BX403747
AQ951683
CR339134
CR339134
CR486489
CG933873
                                                                                                                                                             Score 397.8; DB 11;
Pred. No. 1.2e-80;
Pred. No. 1.2e-80;
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AL069440 Drobophil
BX403747 BX403747
AQ951683 Sheared D
CR339134 mte1-7015
CR46648 mth2-155N
CG933873 MBEDK50TR
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                                                                                                                                 339
                               282
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331 TGAATTTTGATGAGGCACATT-TACCCTTTAGCCCATGTTAACATTTTCTTCAGGATTCA 389	Q Qy
ry Match  36.6%; Score 293.2; DB 11; Length 393; it Local Similarity 91.7%; Pred. No. 1.3e-56; iches 321; Conservative 0; Mismatches 28; Indels 1; Gaps	Query Best Match
/clone="plate=3045 Col=8 Row=K" /clone="plate=3045 Col=8 Row=K" /sex="male" /clone_lib="CIT Approved Human Genomic Sperm Library D" /clone_lib="CIT Approved Human Genomic Sperm Library D" /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"	ORIGIN
Fax: (206) 616-3887  Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3045 row: K column: 8  Class: BAC ends Class: BAC ends High quality sequence stop: 393. Location/Qualifiers 1. 393  source /organism="Homo sapiens" /mol_type="genomic DNA" /db xref="taxon:9606"	FEATURE SO
AL ED	TITLE JOURNAL PUBMED COMMENT
NISM NCE	KEYWORDS SOURCE ORGANISM ORGANISM REFERENCE AUTHORS
	RESULT 2 AQ129390/c LOCUS DEFINITION ACCESSION VERSION
640 AGGCTGTCCTTTTACACCATTTTTAGTCTTTCTG 680	Db Qy
580 AAGAAATTACACAAGTACTAGTTTATTGGTTATTCACGGAGAGTGAGT	D Qy
520 TTTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCC	\$ Q
460 CCACACTGAATATCAAAAGAAATAAAACTAAAATCATTATAAGGACACAACCATGTGATA	g 44
	Db

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RESULT 3
BG204609/c
LOCUS
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AUTHORS
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Tel: 216 431 9900
Fax: 216 361 9596
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activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

1 (bases 1 to 247)

1 (bases 1 to 247)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Cain, S., Leventhal, C., Costanzo, D., McElligott, K., Boozer, S.
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RST24016 Athersys RAGE Library
BG204609
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                      GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 197
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            scain@athersys.com
                                                                                                                                                                  /Clone lib="Atherrys RAGE Library"
/clone lib-"Atherrys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                         xref="taxon:9606"
l_line="HT1080"
                                                                                            10.3%;
                                                                          Score 82.8; D
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s cDNA, mRNA sequence.
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ATTACTTCCTTGTAGATAAGTTCTGT

GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTC

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RESULT 4
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1 (bases 1 to 390)

1 (bases 1 to 390)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Melton, D., Brown, J., Kenty, G., Gradwohl, G., Clifton, S., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Bendocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is29b07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6553861 5' similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10 , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Other_ESTs: is29b07.x1
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                                                                                                                                      /clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_l:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinouepalmgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="Purified pancreatic islet"
/lab_host="DH10B"
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                             10.3%;
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Score 82.8; DB 4;
Pred. No. 2.9e-08;
0; Mismatches 2;
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ATTACTTCCTTGTAGATAAGTTCTTT

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         DEFINITION
                                               AW297251/c
                                                                         RESULT 6
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Matches 84
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                                                                                                                                          39
AW297251 429 bp mRNA linear I
UI-H-BW0-aji-b-12-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVI&t2=QVI-FT0202-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             021100-455-f02&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simpson, A.J.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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QV1-FT0202-021100-455-f02
BF856752
                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                   ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                    GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                            GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 407)
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: prostate tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence stop: 407.
                                                                                                                                                                                                                                                                                                                                              10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lib="FT0202"
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                            Score 82.8; DB 2;
Pred. No. 2.9e-08;
                                                                                                                                                                                                                                                                                                                           Mismatches
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2 FT0202 Homo sapiens cDNA,
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                                                                                                                                                                                                                                                                                                                                                                   Length 407;
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                              EST 16-JAN-2000
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JOURNAL COMMENT
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AUTHORS
TITLE
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SOURCE
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VERSION
Matches
                                 Query Match
Best Local Similarity
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84;
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I.MA.G.E. Consortium/LNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbir.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AW297251
AW297251.1 GI:6703887
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1 (bases 1 to 429)
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   Conservative
                                                                                                                                                                                                                                                                        /Clome lib="NCI CGAP Sub6"
/clome lib="NCI CGAP Sub6"
/clome lib="NCI CGAP Sub6"
/mote="Vector: pT773D-Pac1; Site_1: Not I; Site_2: Eco RI;
/mote-1: Not I; Site_1: 
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                                                                                                                                                                               _LIB=NCI_CGĂP-Lu13
_SEQ=GCCGG"
                                                                                                                                                                                                                                              TISSUE=lung
                                 10.3%;
٥,
Score 82.8; DB 7;
Pred. No. 2.9e-08;
0; Mismatches 2;
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                                                                   Length 429;
       Indels
       0
   Gaps
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626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685

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REFERENCE
AUTHORS
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AA663771
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ORGANISM
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DEFINITION
                                                                                                                                                                 Query Match 10.3%;
Best Local Similarity 97.7%;
                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong Possible reversed clone: polyT not found Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 350.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae: Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA663771
448 bp mRNA linear EST 15-DEC ae68h10.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969379 3' similar to SW:JNK3_RAT P49187 STRESS-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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  ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                        GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACTTCCTTGTAGATAAGTTCTTT
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                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                      /Clone_lib="Stratagene schizo brain S1"
/note="Vector: Bluescript SK.; Site 1: EcoRI; Library
/note="Vector: Bluescript SK.; Site 1: EcoRI; Library
/constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:969379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="schizophrenic brain S-11 frontal lobe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
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                                                                                                                                                               Score 82.8; DB 1;
Pred. No. 2.9e-08;
                                                                                                                                           Mismatches
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                                                                                                                                                                                     DB 1;
                                                                                                                                                                                     Length 448;
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  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UI-E-CK1-agb-1-15-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone UI-E-CK1-agb-1-15-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coordinated Laboratory for Computational University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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319 335 9565
                                                                                                             /tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="PHIOB (Life Technologies) (TI phage resistant)"
/lab_host="PHIOB (Life Technologies) (TI phage resistant)"
/clone_lib="UI-E-CKI"
/clone_lib="UI-E-CKI"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CKI is a normalized CDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTCC. This library was created for the program,
Gene Discovery in the Visual System, supported by National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-E-CK1-agb-1-15-0-UI"
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/db_xref="taxon:9606"
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Eutheria; Euarchontoglires; Primates; Catarrhini;
                         10.3%;
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                         82.8; DB 3
No. 2.9e-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information o
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM508552 BP MRNA linear EST 12-MAI ii37all.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MNS1 MAI musculus cDNA clone IMAGE:5943836 5' similar to SW:KKIO HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:2006708 This sequence now available from the for clone orders contact: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Other_ESTs: ii37all.xl
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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h quality sequence stop: 430.
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                                                               /note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; Five libraries representing EI0.5/12.5 pancreat; bud, E16.5 pancreas; newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6.791-806; 0.5 microgram
single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded
                                                                                                                                                                                                                                                                                                                                      N1-MMS1"
                                                                                                                                                                                                                                                                                                                                                                                  /lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'sex="Both for embryonic & newborn, male for adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:5943836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="ICR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Good hit to opposite strand read. MOUSE-PANCREAS VERIFICATION
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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ik36f03.y5 HR85 islet Homo sapiens cDNA clone IMAGE:5783165 5'
similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Douglas Melton, Klaus H. Kaestner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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ad is a 5' RESEQUENCE of a
/clone_lib="HR85 islet"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_l:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_l:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_lib.
/note="Organ: Pancreas; Vector: pBluescript Sk(-); Site_lib.
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/note="Organ: Pancreas; Vector: pBluescript Sk(-); Site_lib.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5783165"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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Pred. No. 3e-0
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    Query Match
Best Local Similarity
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1 (bases 1 too 618)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Melton,D., Brown,J., Kenty,G., Gradwohl,G., Clifton,S., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hiller,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pannreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library was constructed by Dr. Hiroshi Inoue DNA sequencing by Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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618 bp mRNA linear EST 14-MAY-2002 ik36f33.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5783165 3' sinilar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
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Location/Qualifiers
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                                                                                     NotI; Site 2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size Alkb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127. 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                               /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
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ol_type="mRNA"
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Query Match
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RESULT 12
DR762335/c
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TITLE
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HESC4_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 2089
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: BresaGen, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: La
University of Georgia
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/ Cloud Tibe Nil Not 2.02
/ (note "Net Deby Nil Not 2.1)
/ (note "Net Deby Nil Not 2.2)
/ (note "Net Coll name of Diastocyst stage embryos and the inner cell mass of blastocyst stage embryos and differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BGO1.
Positive for Nestin and Musashi expression. Passage number 18. cDNA primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCAGCGCGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH MGC 259). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Note: this is a Mammalian Gene Collection library."
                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="human embryonic stem cells"
/cell_line="BG01"
/tell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="embryonic stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
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|mol_type="mRNA"
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10.3%;

Score 82.8;

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ACCESSION KEYWORDS VERSION

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BI824308/c
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Best Local S
Matches 84
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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603040725F1 NIH_MGC_115 Homo sapiens
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Plate: LLAM11453 row: a column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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1 (bases 1 to 933)
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BI824308
                                                                                                                                                                                                                                                        Similarity
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                  GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTGAATTC
                                                                       ATTACTTCCTTGTAGATAAGTTCTGT 711
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                                             ATTACTTCCTTGTAGATAAGTTCTTT 17
                                                                                                                                     GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 825.
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                                                                                                                                                                                                                                Conservative
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//clone lib="NIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pool of state library (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5181582"
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mol_type="mRNA"
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                                                                                                                                                                                                                         Score 82.8; DB 2;
Pred. No. 3.1e-08;
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JOURNAL
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Best Local
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                                                                                                                                                                                                                                                                                                                         626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
BG219861
RST39628 Atl
BG219861
BG219861.1
                                                                                                                                                                                                                                                                                                                                                                         83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RZPD; IMAGP998K0612866.

RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPDJ (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101

Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human UnigeneSet -
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 462)
Ebert,L., Heil,O., Hennig,S., Neubert,P.,
Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RZPD Deutsches Ressourcenzentrum
Im Neuenheimer Feld 580, D-69120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo
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                                                                                                                                                                                                                                                                                GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCA
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: PBluescript SK(-); Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, Mp.
Amplified once. Contact information: Hiroshi Inoue, Mp.
Amplified once. (Alan Permutt Lab), Mashington University
Metabolism Div. (Alan Permutt Lab), Mashington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                             Athersys RAGE Library Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGp998K0612866 ; IMAGE:5783165"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                              Score 81.8; DB 4;
Pred. No. 4.9e-08;
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Heidelberg, Germany
                                                                       mRNA
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Seq primer:

Peters, M.,

FEATURES

COMMENT

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mRNA sequence EST 21-APR-2001

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Matches 81
                                             TITLE
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                                                                                1 (bases 1 to 386)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                  3
BF858136
QV1-FT0202-131100-470-c12
BF858136
BF858136.1 GI:12245880
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechmol. 19 (5), 440-445 (2001)
                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Athersys, Inc.
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216 361 9596
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/ibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/cell_line="HT1080"
  Acad. Sci. U.S.A.
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Pred. No. 1e-07;
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FT0202 Homo sapiens cDNA,
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97 (7), 3491-3496 (2000)
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                                                                                                    Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endoorine Pancreas Consortium
Unpublished (2000)
Contart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
Contact: Douglas Melton, Klaus H. Kaestner, & Hirosl
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity &
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB069160 457 bp mRNA linear EST 21-JAN-2003 is13g01.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6364968 3' similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
                                                                                                                                                                                                                                                                                                            Hominidae; Homo.
1 (bases 1 to 457)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV1&t2=QV1-FT0202-
1311100-470-c12&t3=2000-11-13&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rua Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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/db xref="taxon:9606"
/db xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0202"
/note="Organ: prostate tumor; Vector: pucl8; Site_1: SmaI;
/note="Organ: prostate tumor; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Pred. No. 1e-07;
0; Mismatches
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                           Divinity Ave,
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REFERENCE
AUTHORS
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BG194386/c
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RST13533 Ath
BG194386
BG194386.1
EST.
              3201 Carnegie Ave, Cleveland, OH
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 397.
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Torgan: Pancreas; Vector: pBluescript SK(-); Site 1: NotI; Site 2: XhoI; cDNA made by oligo-dT priming.

Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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Pred. No. 1e-07;
0; Mismatches 1;
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Query Match Best Local S Matches 80

h 9.8%; Similarity 97.6%; 80; Conservative

Score 78.8; DB 2; Pred. No. 2.3e-07; 0; Mismatches 2;

Length 257;

Indels

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PUBMED
COMMENT
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AUTHORS
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SOURCE
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BG209408/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 257)

1 (bases 1 to 257)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittlington,J., Lerner,L., Costanzo,D., McBlligott,K., Boozer,S.,
Mays,R., Smith,E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K.
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of genome expression
Nat. Bjotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                         3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Scott J. Cain Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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RST28923 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence
BG209408
                                                                                                                                                                                                                                                                                                                                                       Email: scain@athersys.com
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/mol type="mRNA"
/db Xref="taxon:9606"
/cell line="HT1080"
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/clone lib="Athersys RAGE Library"
/clone sib="See 'Creation of Genome-wide Protein Expression Inbraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
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/clone lib="Athersys RAGE Library"
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/note="Gee 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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Pred. No. 1
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L.1e-07;
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836 bp mRNA linear EST 06-OCT-2005
CJ443965 macaque brain cDNA library QccE Macaca fascicularis cDNA
clone OccE-21545 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Division of Biomedical Resources
National Institute of Biomedical Innovation
Saito-Asagi 7:6-8, Ibaraki, Osaka, 567-0085,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirata, M., Suzuki, Y., Sugano, S. and Hashimoto, K. Macaca fascicuraris cDNA database Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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CJ443965.1 GI:77250642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nosada@nibio.go.jp
URL: http://genebank.nibio.go.jp/gbank/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-72-641-9811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Naoki Osada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecidae;
                                                                                                                                             GCACCTGAAGGAGAAGGCTGTCCTTTTACTACGCCATTTTTAGTCTTCTTCTTGAGTTC
                                                                                                                                                                       GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                              ATTACTTCCTTGTAGATAAGTTCTTT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                      /clone_lib="macaque brain cDNA library OccE"
/note="Vector: pME18S-FL3 (Acc.No. AB009864); Site_1:
DrailI (CACTGTGTG); Site_2: DrailI (CACCATGTG); lst strand
cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
synthesized using specific 5' and 3' primers and amplified
by PCR. The PCR product was digested with Stil and size
selection was performed to exclude fragments <1.5kb.The
Sfil-digested PCR product was cloned into distinct DrailI
sites of pME18S-FL3. XhoI sites just outside the DrailI
sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="cerebellum cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'sex="male"
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                                                                                                                                                                                                                        Score 78; DB 5; Le
Pred. No. 3.9e-07;
0; Mismatches 5;
                                                                                                                                                                                                                                                               Length 836
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RESULT 22
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RESULT 21

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REFERENCE
AUTHORS
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TITLE
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Neuherberg, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project This clone
(DKFZp459H0638) is available at the RZFD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZFD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459H0638
Further information about the clone and the sequencing project is
available at http://mlps.gsf.de/projects/cdna/.
                                                                                           1775
1715 CTTCCTTGTAGATAAGTTCTTT 1694
                                            690
                                                                                                                                     630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                                                                                                    79;
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Koehrer,K., Beyer,A., Mewes,H.W.,
Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pongo pygmaeus
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                       CTTCCTTGTAGATAAGTTCTGT 711
                                                                                         CTGAAGGAGAAGGCTGTCCTTTTACTACGCCATTTTTAGTCTTTTCTTCTGAGTTCATTA
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                    VRHKILFPGRDYIDQMNKVIBQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFP
DSLFPADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVMYDPAEVEAPP
PQIYDEQLDEREHTIDEWKELIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ"
                                                                                                                                                                                                                                                                                                                                                                            /trānslation="MSKSKVDNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIYCAAY
DAVLDRNVALKKLSRPFQHQTHAKRAYRELVLMKCVNHKNIISLLNVFFTPQKTLEGFQ
DVYLVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKFDSNIVK
SDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="cortex"
/clone_lib="459 (synonym: pcor1). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="hypothetical protein"
/protein_id="CAH91384.1"
/db_xref="GI:55729297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="DKFZp459H0638"
638. .1792
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sapiens), differentially spliced"
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/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp459H0638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="DKFZp459H0638"
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                                                                                                                                                                                                           9.7%;
96.3%;
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                                                                                                                                                                                                           Score 77.2; DB 6; Pred. No. 6.5e-07;
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                                                                                           1716
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JOURNAL COMMENT
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ORGANISM
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Best Local S
Matches 80
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                                                                                                                                                                                                                                                                       420
                                                                                     CJ491725 MACAQUE testis cDNA library QtsA Macaca fascicularis cDNA clone QtsA-19671 5', mRNA sequence.

CJ491725 CJ491725 GI:77292599

EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                    Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville,
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1678 Std Error: 0.00
Seq primer: T7: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yi,Y., Desai,R., Olarte,M.
Expressed sequence tags fr
Unpublished (2003)
Other ESTs: CH3#056_B08T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF408692 946 bp mRNA linear EST 02-SEP-20-CH3#056_B08T7 Canine heart normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH3#056_B08 5', mRNA sequence.
CF408692
CF408692.1 GI:34409938
EST. familiaris cDNA clone CH3#056_B08 S', mRNA sequence.
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Division of Genetic Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canida
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                            ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue soutce: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="Canine heart normalized cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="heart"
|dev_stage="mixed developmental stages (adult, 30 day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Canis familiaris"
|mol_type="mRNA"
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clone="CH3#056_B08"
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ce tags from Canine hear
                                                                                                                                                                                                                                                                                                                                                                                                                0
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Pred. No. 9.1e-07;
0; Mismatches 6;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Osada,N., Hida,M., Kusuda,J., Tanuma,R., Hirata Suzuki,Y., Sugano,S. and Hashimoto,K. Macaca fascicuraris cDNA database Unpublished (2005)
Contact: Naoki Osada Division of Biomedical Resources National Institute of Biomedical Innovation Saito-Asagi 7-6-8, Ibaraki, Osaka, 567-0085, Jarel: 81-72-641-9911
Fax: 81-72-641-9916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nosada@nibio.go.jp
URL: http://genebank.nibio.go.jp/gbank/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 818)
                                                                                                                                   /clone lib="macaque testis cDNA library QtsA"
/note="Vector: pME185.FL3 (Acc.No. AB09864); Site 1:
/note="Vector: pME185.FL3 (Acc.No. CACCATGTG); 1st strand
cDNA was primed with an oligo(dT) primer
{ATCTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
synthesized using specific 5' and 3' primers and amplified
by PCR. The PCR product was digested with Sfil and size
selection was performed to exclude fragments <1.5kb.The
Sfil-digested PCR product was cloned into distinct DrallI
sites of pME185.FL3. XhoI sites just outside the DralII
sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="testis"
/dev_stage="adult"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="QtsA-19671"
                        9.4%;
Score 75.6; DI
Pred. No. 1.4e.
0; Mismatches
                           ; DB 5;
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Conservative

Gaps

sequence. DA807178 DA807178.1 i (bases) to 568)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, T., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes DA807178 DA807178 OCBBF3 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens (human) Hominidae; Homo. Homo sapiens bp mRNA linear E EST 11-NOV-2005 4 5', mRNA Wagatsuma, M.,

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JOURNAL
PUBMED
COMMENT
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AUTHORS
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BF857793
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635
                                                                                                                                                                                                                                                                                                       1 (bases 1 to 408)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2705//33 408 bp mRNA linear QV1-FT0202-071100-465-a04 FT0202 Homo sapiens cDNA, BF857793
                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
Project. This entry can be seen in the following URL
                                                                                                                                                                                                  Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF857793.1 GI:12245537
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NEDO human cDNA project (New Energy and Industrial Technology

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one

pass sequencing: RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helix Research Institute
2-6-7 Kazusa Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 16 (1),
16344560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                  +55-11-2704922
+55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
/dev_stage="fetal"
/clone_lib="OCBBF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OCBBF3022734"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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Pred. No. 1.5e-06;
0; Mismatches 1;
                                                                                                                                                                                                                                         97 (7), 3491-3496 (2000)
                                                                                                                                4 andar, 01509-010,
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AW314598/c
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                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 423)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                               Single pass sequencing. Bases ov 0.980904.e. Vector identified and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                                     Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-FT0202-071100-465-a04&t3=2000-11-078t4=1)
Seq primer: put la forward
High quality sequence stop: 325.
                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 9 row: D column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
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EST.
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                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
                                                                                                                                                                        PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                11282978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (cattle)
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Similarity 90.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTACTTCCTTGTCGATTAGTTCTTT 393
                                                                                    te: 9 row: D column: 1
primer: ATTTAGGTGACACTATAG
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/note="Organ: prostate tumor; Vector: pucl8; Site 1: Smal; Amain: prostate tumor; Vector: pucl8; Site 1: Smal; Site 2: Smal; Amini library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                               Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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Pred. No. 4.6e-06;
0; Mismatches 8
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                                                                                                                                                                                                                      cross_match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts, A.J., Stone, R.T., ahrenkrug, S.C.,
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RESULT 27
DN543033/c
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JOURNAL
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Best Local Similarity
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Best Local Similarity
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 686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with
trimmed with the aid of the trim_alt optio
cross_match v0.990329.
Plate: RLK8072 row: G column: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith, T.P.L., Roberts, A. Wray, J.E. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DN543033.1 GI:61001631 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1391834 MARC 7BOV Bos taurus
DN543033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (cattle)
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                                 GCACCTGAAGGAAAGGCTGTCCTTTCACAACGCCATTCTTCGTCTTTTCTTCCGAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                    ce: RLK8072 row: G column: 21 primer: GTAATACGACTCACTATAGGG.
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                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARS, US Meat Animal Research Center x 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC_780V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from day 20 and day 40 embryos."
                                                                                                                                                                                    /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC_4BOV
                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    organism="Bos taurus"
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                                                                                                                  8.8%;
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                                                                                                                  Score 70; DB 9;
Pred. No. 2.6e-05;
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Pred. No. 2
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2.5e-05;
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on. Vector identified with
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KEYWORDS
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BE752856/c
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BE752838/c
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                                                                                                                                                                                     686 ATTACTTCCTTGTAGATAAGTTCT 709
                                                                                                                                                                                                                                                                626 GTACCTGAAGGAGAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                             28
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BE752838 551
205425 MARC 2BOV Bos taurus
BE752838 BE752838.1 GI:10166830
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., (Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205445 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE752856
BE752856.1 GI:10166848
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Plate: 46 row: P column: 1
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FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                         /lab_nobl= ...../
/clone_lib=MARC_2BOV"
/clone_Tib=MARC_2BOV"
/notee="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913".
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Pred. No. 3.1e-05;
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                                                                                                                                                                                                                                                                                                      sequence.
DV915617
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1 (bases 1 to 916)
Moore, S., Alexander, L., Browns
Tanaguchi, M., Wang, Z., Yu, J.,
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                              DV915617.1
EST.
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PO Bo:
Tel:
                                                                                                                                                                                                                                                                                                                                                              LB0288.CR_F16
                                                                                                                                                                                   Bos taurus
                                                                                                                                                                                                                  Bos taurus (cattle)
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Plate: 46 row: M column: 8
Seq primer: ATTTAGGTGACACTATAG.
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Single pass sequencing. Bases ca.
v0.980904.e. Vector identified by
and _minmatch 12 options.
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Box 166, Clay Center, N
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402 762 4390
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/mol type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI, Site 2: 9a
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
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   Brownstein, M., Gv
Yu, J., Prange, C.,
                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
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NE 68933-0166, U
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   Guan, L., Lobo, S., Meng, Y., Schreiber, K., Shenmen, C.
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 801)

2 (bases 1 to 801)

3 (bases 1 to 801)

3 (bases 1 to 801)

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BC Cancer Agency
Suite 100, 570 West 7th Avenue,
Canada, V5Z 4S6
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LB0287.CR_A06 GC_BGC-28 Bos taurus cDNA clone IMAGE:8222096, mRNA
                                                                                                       Canada's Michael Smith Genome Sciences Centre
                                                                                                                                   Unpublished (2005)
Contact: Robert Kirkpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (cattle)
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Contact: Robert Ki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: robertk@bcgsc.ca
Insert Length: 916 Std Error:
Plate: LB0288 row: F column: 1
High quality sequence stop: 916.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canada's Michael Smith Genome Sciences Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Cerebral cortex"
/dev_stage="8.5 months old calf"
/lab_host="E. coli DH10B T1 Phage resistant"
/clone_lib="GC_BGC-28"
/note="Organ: Cerebral cortex; Vector: pExpress 1; Site_1:
/note="Organ: Cerebral cortex; NotI (3' end of cDNA)"
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/clone="IMAGE:8222610"
/sex="female"
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/strain="L1 Hereford"
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87.2%;
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                                      Vancouver, British Columbia,
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BY126616/c
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CE 1 (bases 1 to 332)

RS (bazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Matsuda, H., Lim, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K. S., Gaasterland, T., Garibooldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D. R., Manata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Petrasid, R. M., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Vang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zinmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zinmer, A., Carninci, P., Hayattsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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332 bp mRNA linear ES
BY126616 RIKEN full-length enriched, adult male brain
CDNA clone L630049C19 5', mRNA sequence.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 1-604-707-5900 x5406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTTTCTTCCGAGTTCATTACTTCCTTATAGATAAGTTCTTT 539
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/dev stage="8.5 months old calf"
/lab_host="E. coli DH10B TI Phage resistant"
/clone lib="GC BGC-28"
/note="Organ: Cerebral cortex; Vector: pExpress 1; Site_1:
/note="Organ: Cerebral cortex; Vector: perpress 1; Site_1:
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'clone="IMAGE:8222096"
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Pred. No. 5e-05;
0; Mismatches 22;
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Score 68.4; DB 4; Pred. No. 5.8e-05; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. halysis of the mouse transcriptome based on functional annotation halysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                    /clone lib="RIKEN full-length enriched, adult male brain"
/note-"Site 1: Sall; Site 2: BamHI; CDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. Istrand cDNA was
grand with a primer [5'
GAGAGAGAGAGAGCCTCTTTTTTTTTTTTTTTTVN 3'], CDNA was
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B"
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/clone="L630049C19"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating as small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 427-537, >(CA)n#Simple_repeat
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EST.
Mus musculus (house mouse)
Mus musculus
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Bonaldo, M.F.,
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UI-M-AH0-acy-e-12-0-UI.rl NIH BMAP_MCE Mus musculus cDNA
UI-M-AH0-acy-e-12-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                          GCACCTGAAGGCGAGGGCTGGCCTTTGACTACGCCATTCTTAGTCTTCTCTTCTGAGTTC
                                                                                                                                              GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
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/clone="UI-M-AHO-acy-e-12-0-UI"
/clone="BI-M-AHO-acy-e-12-0-UI"
/dev stage="27-32 days"
/lab host="PH10B (Life Technologies)"
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/clone_lib="NII_BMAP MCE"
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791-806, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories."
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/strain="C57BL/6J"
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Pred. No. 6e-05;
0; Mismatches 11;
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8.6%;

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BU743848/c
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McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M., Ritter, E., Tsagareishvili, R., Ronko, I., Maguire, L., Kennedy, S., Bennett, J., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU743848 553 bp mRNA linear EST 21-APR-200 mai49dll.yl McCarrey Eddy round spermatid Mus musculus cDNA clone IMAGE:6449444 5' similar to SW:MKIO_HUMAN P53779 MITOGEN-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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                                                                                                                                                                                     /tissue_type="round spermatids, pooled from multiple mice"
/dev stage="60 day"
/lab_host="PH108 (phage-resistant)"
/clone_lib="McCarrey Eddy round spermatid"
/clone_lib="McCarrey Eddy round spermatid"
/note="Organ: testis; Vector: pBluescript SK+
/note="Grant testis; Vector: pBluescript Sk+
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/strain="CD-1"
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ced. No. 6e-05;
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RESULT 36
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CB234404/c
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AK042368 2343 bp mRNA linear HTC 02-SEP-2005 Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630085G12 product:mitogen activated protein kinase
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CB234404
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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CB234404.1 GI:28285982
EST.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: T. Rajendra Kumar and Martin M. Matzuk
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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http://image.llnl.gov
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//lab host="DH10B (phage-resistant)"
//lab host="DH10B (phage-resistant)"
//clone="lib="NIH MGC_166"
//clone=lib="NIH MGC_16
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/db_xref="taxon:10090"
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Pred. No. 6.2e-05;
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The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1563 (2005)

B (bases 1 to 2343)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Ohsaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakaume, N., Sagabe, Y., Tagawi, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Tomaru, A., Toya, T., Yasunishi, A.,
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Direct Submission
Submitted (16-70UL-2001) Yoshihide Hayashizaki, The Institu
Physical and Chemical Research (RIKEN), Laboratory for Gen
Exploration Research Group, RIKEN Genomic Sciences Center
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Genome Exploration Research Group, Genome Science (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)
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Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
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AK042368.1 GI:26335078
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                                                                                         Institute of for Genome
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230-0045, Japan (E-mail;genome-res@gsc.riken.jp.

Yokohama

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                                                                                                                                             AK036275
AK036275.1 GI:26085131
HTC; CAP trapper
Mus musculus (house mouse
Mus musculus
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                          AK036275 PRIMA Linear AK036275 PRIMA Linear Mus musculus 16 days neonate cerebellum cDNA, RIKEN enriched library, clone:96030051C24 product:mitogen protein kinase 10, full insert sequence.
Carninci, P. and Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                         musculus (house mouse)
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/db_xref="GI:26335079"
/translation="MSLHFLYYCSEPTLDVKIAFCQGFDKHVDVSSIAKHYNMSKSKV/translation="MSLHFLYYCSEPTLDVKIAFCQGFDKHVDVSSIAKHYNMSKSKV/translation="MSLHFLYYCSEPTLDVKIAFCQGIVCAAYDAVLDRNVAIKKLSRPFQNQDNQFYSVEVGDSTFTVKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQNQTDNANLCQVIQMETAKRAYRELVLMKCVNHKNIISILNVFTPQKTLEEFQDVYLVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMGYKENVIJMSVGCIMGEMVRHKILFPGRDYIDQMKVI
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2323. .2328
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LLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKGQPSPSGAAVNSSESLPPSSSVNDISSMSTDQTLASDTD
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132. .1526
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
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db_xref="taxon:10090"
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                                                                                                                                                                                                                                                     Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohana Institute; 1-7-22 Suehiro-cho, Tsurumi ku, Yokohan Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                     URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigeromic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                   prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Science Group (Genome Network Project Core Group)
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)
B. (bases 1 to 2729)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Genome Exploration Research Group, Genome Science (Genome Network Core, Team) and the FANYOM Consortium. Antieense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium, the RIKEN Genome Exploration Research Group
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                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-FN0210-
301000-001-blo&t3=2000-10-30&t4=1)
Seg primer: puc 18 forward
High quality sequence stop: 559.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 561)

1 (bases 1 to 561)

Dias Neto, E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Dias Neto, E., Garcia Correa,R., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher, P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/dev_stage="16 days neonate"
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/clone Tib="RIKEN full-length enriched
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'db_xref="taxon:10090"
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87.2%;
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Mus musculus (house mouse)
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/clone_lib="Gran: prostate_normal; Vector: puc18; Site_l:
/note="Organ: prostate_normal; Vector: puc18; Site_l:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
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Pred. No. 8.3e-05,
0; Mismatches
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Fantawa, T., Satonishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

TM FANTOM Consortium
Sessa, L., She
Sinclair, B.,
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Sperling, S., Stupka, E., Sugiura, K., Sultana, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegger,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabaroveky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katesyama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagishira,N., Kojima,M., Kodo,S., Konno,H., Nakano,K., Niomiya,N., Nishio,T., Okada,M., Kodo,S., Konno,H., Nakano,K., Niomiya,N., Nishio,T., Okada,M., Watahiki,A., Okamura-Oho,Y., Suzuki,B., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hori, F., Iida, J., Imamura, K., Motani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genome Exploration Research Group
Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16141073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FANTOM Consortium
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                           /protein_id="BAE37234.1"
/db_xref="G1:74190276"
/db_xref="G1:74190276"
/translation="MSLTFLYYCSEPTLDVKIAFCQGFDKHVDVSSIAKHYNMSKSKV
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DNQFYSVEVGDSTFTVLKRYQNLKFIGSGAQGIVCAAYDAVLDRNVAIKKLSRFFQNQ
THAKRAYRELVLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQME
                                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product; mitogen activated protein
kinase 10 (MGD|MGI:1346863 GB|BC046625, evidence: BLASTN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
LDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSE
                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="7 days neonate"
518. .1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="cerebellum"/clone_lib="RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="FANTOM_DB:A730093C22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="A730093C22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,
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ORIGIN

Matches

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Query Match
Best Local S
Matches 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMGNNUC:NRDG1-00127-G9-A nrdg1 (10855)
nrdg1-00127-g9 5', mRNA sequence.
CB607972
CB607972.1 GI:29547657
EST.
CF535846 570 bp
UI-M-GHO-cha-a-06-0-UI.rl NIH BMA
IMAGE:30533669 5', mRNA sequence.
CF535846 GI:34587814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amgen EST Program
Amgen Rat EST Program
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                     GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTC
                                                                                                                                                                                                                                              ATTACTTCCTTGTAGATGAGTTCTTT 353
                                                                                                                                                                                                                                                                                  ATTACTTCCTTGTAGATAAGTTCTGT
                                                                                                                                                                                                                                                                                                                                                      GCACCTGAAGGTGAGGGCTTGGCCTTTGACTACGCCGTTCTTAGTCTTCTCTTCTGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGAGTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTCATTACCTCCTTGTAGATAAGTTCTTT 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTCATTACTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amgen Center Drive, Thousand Oaks, 805 447-4881
te: 00127 row: g column: 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="nrdg1-00127-g9"
/tissue_type="Dorsal Root Ganglia"
/clone_Tib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; ratdorsal root ganglia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYIDQWNKVI
EQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKE
LIYKEVMNSEEKTKNGVVKGQPSPSA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66.8; DB 4;
Pred. No. 0.00014;
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Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 576;
                                                                                    musculus
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                              ACCESSION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                                                                                                                                                           630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
                                                                                                    BM944347
UI-M-EHOp-bvq-f-13-0-UI.r1 NIH E
IMAGE:5695500 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                              BM944347.1
EST.
                                                                                    BM944347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following repetitive elements were found in sequence: 383-493, >(CA)n#Simple_repeat Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Muridae; Murinae; Mus. 1 (bases 1 to 570)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                        CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                           CTGAAGGCGAGGGCTGGCCTTTGACTACGCCATTCTTAGTCTTCTCTGAGTTCATTA
                                                                                                                                                                                                                                                                                                   CCTCCTTGTAGATAAGTTCTTT 102
        musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev stage=1, 5, and 15 days newborn"
/lab_nost="PH108 (T1 phage resistant)"
/clone_lib="NIH_BMAP_CH0"
/clone_lib="NIH_BMAP_CH0"
/note="Corgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Corgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Corgan: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/note="Corgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Corgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Corgan: Brain; Vector: pYX- Asc; Schome Research, 6:791-806,
/note="Corgan: Brain; Vector: pXX- Asc; Constructed on a 1% agarose
/note="Corgan: Brain and CDNA was size selected according to mRNA size fraction, ligated
/note="Corgan: Brain; Vector: pxx- Asc; Vector: The library tag
/note="Corgan: Brain Anatomy Project (BMAP): 'Gene Discovery in the
/note="Corgan: Brain Anatomy Project (BMAP): 'Gene Discovery in the
/note="Corgan: Brain Anatomy Project (BMAP): 'Gene Discovery in the
/note="Corgan: Brain Anatomy Project (BMAP): 'Gene Discovery in the
/note="Corgan: Brain Anatomy Project (BMAP): 'Gene Discovery in the
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/note="Corgan: Brain Anatomy Project (BMAP): 'Gene Discovery in the
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/strain="C57BL/6"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="IMAGE:30533669"
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                                                          GI:19427932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB
Pred. No. 0.00
0; Mismatches
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                                                                                                                                   BMAP EHOP Mus
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                                                                                                                                                                  mRNA
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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RESULT 40 CB607972/c LOCUS

this cDNA

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ORGANISM

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RESULT 41 CF535846/c LOCUS

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CX221469/c
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                                                                                                        CX221469 639 bp mRN
MNS38129 Mouse Neurosphere Normalized
cDNA 5', mRNA sequence.
CX221469 CX221469 CX221469.1 GI:56876761
EST.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammaila; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAAGGCGAGGGCTTGGCCTTTGACTACGCCATTCTTAGTCTTCTTCTGAGTTCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCTTGTAGATAAGTTCTGT 711
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/dev stage="embryo 18.5 dpc"
/lab_host="DH108 (TI phage resistant)"
/clone_lib="NIH_BMAP_EHOP"
/clone_lib="NIH_BMAP_EHOP"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR_I;
/note="Organ: brain; Senome Research, 6:791-806,
/note="Organ: brain; Vector: pyX-Asc; Vect
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|mol_type="mRNA"
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Pred. No. 0.00021;
0; Mismatches 10
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CF951683/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337
                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF951683 721 bp mRNA linear UI-M-HLO-cnc-a-15-0-UI.rl NIH_BMAP_HLO Mus musculus IMAGE.30633902 5', mRNA sequence.
The following repetitive elements were sequence: 409-519, >(CA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murodea; Muridae; Murinae; Mus.
1 (bases 1 to 721)
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Seg primer: M13REW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 Stockholm, Sweden Tel: +46855378332.
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Contact: Williams, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCCTTGTAGATAAGTTCTTT 316
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/note="Organ: Adult brain; Vector: pcfWSport6.0; A cDNA
library was constructed in pcMVSport6.0 from RNA isolate
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/ResGen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"
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/mol_type="mRNA"
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Seq primer: pYX-5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72;
                                                                                                                                                         Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa

CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 740)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM943588 740 bp mRNA linear EST 14-MAR UI-M-EM0-bvm-m-16-0-UI.rl NIH_BMAP_EM0 Mus musculus cDNA clone IMAGE:5694135 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999
                                                sequence: 498-608, > (CA) n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                            The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCCTTGTAGATAAGTTCTTT 128
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                      primer: pYX-5
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                                                                                                                                  clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site .Double strand cDNA was size selected according to mRNA size fraction , ligated with EcoR I adaptor , digested with NotI and then cloned directionally into pYX-Asc vector . The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP); 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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/lab_host="HH108 (Tl phage resistant)"
/lab_host="HH108 (Tl phage resistant)"
/clone lib="NIH BMAP HL0"
/note="Organ: Head; Vector: pYX-Asc; Site_1: EcoR I;
/note="Organ: Head; Vector: pYX-Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
  Location/Qualifiers
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Pred. No. 0.00022;
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                                                                                                                                                                                                                                                                     Unpublished (2004)
On Feb 2, 2005 this sequence version replaced gi:58509682.
Other_ESTs: JGI CAAL8222.fwd
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel, Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipio Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 802)
Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C. Brokstein, P. and Lindquist, E.A.

DOE Joint Genome Institute Xenopus tropicalis EST project
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JGI_CAAL8222.rev NIH_XGC_tropBrn4 Xenopus tropicalis cDNA clone
IMAGE.7666337 3', mRNA sequence.
                                                                            Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
                                                                                                                                                                                                                     Tel: 925 296 5600
Fax: 925 296 5710
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/(lab host="Did" in Jage resistant)"

/(clone lib="NIH BMAP EMO"

/(clone lib="NIH BMAP EMO"

/(note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIWH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
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/lab_host="DH10B (T1 phage re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="whole brain"
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Pred. No. 0.00022;
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BP485311
BP485311.1 GI:85969903
EST.
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BP485311 Rattus norvegicus pancreatic islet Rattus norvegicus cDNA clone RBC20650 5', mRNA sequence.
                                                                                                                                                          Laboratory of Molecular Genetics
Institute for Molecular and Cellular Regulation,
Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, J
Tel: 81-27-220-8832
                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                              Takeda, J., Wang, H. and Horikawa, Y. Expression profile of mRNAs from rat Unpublished (2006)
                                                                                                                                                                                                                               Contact: Yukio Horikawa
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
                                                                                                                         Email: yhorikaw@showa.gunma-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.

Plate: CAAL 0085 row: 1 column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
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                                                                                                                                             81-27-220-8889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pancreatic islet"
                    /db_xref="taxon:10116"
/clone="RBC20650"
                                                   organism="Rattus norvegicus"
|mol_type="mRNA"
                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7666337"
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Pred. No. 0.00022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO Box 88, Manchester, M60 1QD, Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 331)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Corr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simon Hubbard Department of Biomolecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Simon.Hubbard@umist.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Manchester Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMIST)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01612360409
                                                                                                     /dev stage="16 day embryo"
//lab host="DH10B"
//clone_lib="CSEQCHN57"
/clone_lib="CSEQCHN57"
/clone_lib="CSEQCHN57"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="ChEST780f8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Gallus gallus"
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Score 64; DB 3; Li
Pred. No. 0.00059;
0; Mismatches 5;
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Pred. No. 0.0005;
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                                          Length 331;
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Query Match Best Local

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8.0**%**;

Indels

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Gaps

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RESULT 50
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AUTHORS
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                                                                                                    CX143962 645 bp mRNA linear EST 03-JAN-
1233656 NCCCWA O3RT Oncorhynchus mykiss cDNA 3', mRNA sequence
CX143962 CX143962 1 GI:57000617
EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 645)
                                                                  Oncorhynchus mykiss (rainbow Oncorhynchus mykiss
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1 (base 1 to 778)

Nobica V China; T Vinnia T Navita T Tindo T and Taboda U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryzias latipes (Japanese medaka)
Oryzias latipes
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BJ725204.1 GI:45266296
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T.
Medaka EST Project in Takeda's lab
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MF01FFA035b01"
/sex="mixture of female and
/tissue_type="whole embryo"
/dev_stage="fry stage 40"
/clone_lib="MF01FFA cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryzias latipes"
/mol_type="mRNA"
/strain="Hd-rR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                        7.48;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 2; Ler
Pred. No. 0.0089;
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latipes.cDNA clone MF01FFA035b01 3',
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Plate: 116 row: J column: 6
Seq primer: GTAATACGACTCACTATAGGG
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Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
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Contact: Rexroad CE
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/mol type="mRNA"
/db_xref="taxon:8022"
/tissue_type="pooled"
/lab_host="DH10B"
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/note="Vector: pBluescript SK+; This is a normalized (Cotonote: Vector: pBluescript SK+; This is a normalized (Cotonote: State of the s
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Search completed: July 19, 2006, 20:15:06 Job time : 4924 secs

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1: /EMC Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*

3: /EMC Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

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Sequence 37, Appli
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Sequence 34, Appli
Sequence 27, Appli
Sequence 177, Appli
Sequence 177, Appli
Sequence 174, Appli
Sequence 174, Appli
Sequence 178, Appli
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APPLICANT: McKay, Robert A.
APPLICANT: McKay, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Mero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 178
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapien
US-09-130-616-178
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Best Local Similarity
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
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APPLICANT: Zhou-Liu, Qing
APPLICANT: Zhou-Liu, Qing
APPLICANT: Desanlis-Cremond, Francine
TITLE OF INVENTION: Polypeptides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650B
CURRENT FILING DATE: 2001-07-19
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APPLICANT: Fournier, Alain
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
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US-09-949-016-13753
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0; Mismatches
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: OF BLOOD CELL GENE
                                                                                                                   Matches
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Patent No. 66
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Best Local Similarity 97.7%;
                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 845-41 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORIEY AGENT INFORMATION:
ANAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 POI
CITY: PALO ALTO
STATE: CALIFORNI
                                                                                                                  Local Similarity 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                LENGTH: 1505 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
                                                                                                                                                                                                                                                                             nucleic acid
ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                        GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                   GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09023655
                                                                                                                                                                                                                                                                                                                                                 (650) 845-4166
                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                 10.3%;
                                                                                                                   <u>,</u>
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                                                                                                                Score 82.8; DB 3;
Pred. No. 4.1e-11;
0; Mismatches 2
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                                                                                                                                                    DB 3;
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                                                                                                                                                  Length 1505;
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                                                     1264
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RESULT 5
US-09-165-522-3/c
US-09-165-522-3/c
; Patent No. 6943000
; GENERAL INFORMATION:
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US-09-165-522-1/c
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Best Local S
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Coding Sequence LOCATION: 68...1459
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOPTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-OCT-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                        1263
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                         1323 GCACCTGAAGGAGAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                        ATTACTTCCTTGTAGATAAGTTCTTT 1238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1505 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                             Conservative
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Kuan, Chia-Yi
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Rakic, Pasko
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l, Richard A.
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Pred. No. 4.1e-11;
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US-09-566-921-34/c
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SOFTWARE: PER
SEQ ID NO 34
LENGTH: 2677
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Patent No. 6682888

GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
APPLICANT: Edwards, Carla M.
APPLICANT: Edwards GENES EXPRESSED IN ALZHEIMER'S DISEASE
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEMGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                        Sequence 34, Application US/09566921 Patent No. 6682888
                      FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: LBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     1419 ATTACTTCCTTGTAGATAAGTTCTTT 1394
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MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                               686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTTCTTCTGAATTC
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PERL Program
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STATE: MA
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Whitmarsh, Alan
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US-09-130-616-177/c
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APPLICANT: Desanlis-Cremond, Francine
FILE PETENCE: ST99003-US-CNT-1
CURRENT APPLICATION UNMEER: US/09/909,650B
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION UNMEER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR PRILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-20
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                                                                      GENERAL
                                                                                     Sequence 177, Application US/09130616C Patent No. 6221850
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/09909650B Patent No. 6649388
                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
Matches 84; Conserv
       ENERAL INFORMATION:

APPLICANT: McKay, Robert A.

APPLICANT: Dean, Nicholas M.

APPLICANT: Monia, Brett
APPLICANT: Nero,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aventis Pharmaceuticals Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: homo sapiens
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                                                                                                                                                                                             1219 CTTCCTTGTAGATAAGTTCTTT 1198
                                                                                                                                                                                                                                                                    1279 CTGAAGGAGAAGGCTGTCCT
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                                                                                                                                                                                                                           CTTCCTTGTAGATAAGTTCTGT 711
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97.7%;
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Pred. No. 4.8e
0; Mismatches
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Pred. No. 1.6e-10;
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LENGTH: 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6943000
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GAATGE, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                   CURRENT APPLICATION UMBER: US/09/165,522
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: JNK3 MODULATORS AND NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1343 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1284
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                       TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
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                                       ENGTH: 1773 base pairs
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Flavell, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitmarsh, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rakic, Pasko
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Pred. No. 1.7e-10;
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                                                                                                                                                                                 10363/005001
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RESULT 11
US-09-130-616-174/c
; Sequence 174, Application US/09130616C
; Patent No. 6221850
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; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c',
US-09-771-161A-87
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Matches
                                                                                                                                   GENERAL INFORMATION:
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LENGTH: 2131
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Best Local Similarity
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
                                                      APPLICANT: MCKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Local Similarity 98.8%;
hes 81; Conservative
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SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                CTTCCTTGTAGATAAGTTCTTT 1144
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ilarity 98.8%;
Conservative
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Pred. No. 1.8e-10;
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Pred. No. 1.7e
0; Mismatches
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; LIBRARY: GENBAI
; CLONE: 9468150
US-09-016-434-1389
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                             TELEFAX: (650) 845-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ISPH-0316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                       TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                     TOPOLOGY:
                                                                                     STRANDEDNESS:
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                                                                                                                    ENGTH:
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CALIFORNIA
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Pred. No. 1.8e-10;
0; Mismatches 1
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US-09-165-522-6/c
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                                                                                                                            Matches
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS; double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09165522 Patent No. 6943000 GENERAL INFORMATION:
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Best Local
                                                                                                                                       Local
                                                                                                                                                                                                         MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECONMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1475
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                               690
                                                                                     630 CTGAAGGAGAAGGCTGTCCTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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                                                                                                                                           Similarity
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CTTCCTTGTAGATAAGTTCTTT 1394
                       CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
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                                                                                                                             Conservative
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                                                                                                                                         10.1%;
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                                                                                                                                         Score 80.4; DB 3;
Pred. No. 1.8e-10;
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                                                                                                                             Mismatches
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                                                                                                                                                        Length 2372;
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                                                          RESULT 15
US-09-566-921-33/c
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                          Sequence 33, Application US/09566921
Patent No. 6682888
APPLICANT: Loring,
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, NAME/KEY: Coding Sequence;
; LOCATION: 224...1489
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-165-522-7
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US-09-165-522-7/c
                                                                                                                                         Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09165522 Patent No. 6943000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Passe, J. Peter
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
 1415
                                                                      1475
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAN: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                   690
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                                                                                         630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTCATTA 689
                    CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                LENOTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                      CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA
CTTCCTTGTAGATAAGTTCTTT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
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                                                                                                                                           Conservative
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ll, Richard
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                                                                                                                                         Score 80.4; DB 3;
Pred. No. 1.8e-10;
0; Mismatches 1
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Jeanne F.

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RESULT 17
US-09-165-522-9/c
; Sequence 9, Application US/09165522
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US-09-130-616-175/c
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; OTHER INFORMATION: Incyte ID No. 6682888 413797.7
; NAME/KEY: unsure
; LOCATION: 1770-1816
; OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.1%;
Best Local Similarity 98.8%;
Matches 81; Conservative
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 175
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CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03 NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gearde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McKay, Robert A. APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1975
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 2982
                                                                                                                                                                               1505
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                                                                                                                                       686 ATTACTTCCTTGTAGATAAGTTCTGT 711
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GENES EXPRESSED IN ALZHEIMER'S DISEASE
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                                                                                                                                                                                                                                                                      Score 66.8; DB 3
Pred. No. 4.4e-07
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                        Length 1975;
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NAME/KEY: Coding Sequence;
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LOCATION: 364...1641;
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-165-522-9
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Best Local S
Matches 74
                                                                                                                    Sequence 176, Application US/09130616C Patent No. 6221850 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Davis,
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
                                                                              APPLICANT: McKay, Robert PAPPLICANT: Dean, Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                    Local S. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NUMBER: J. PASTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                            1445 ATTACTTCCTTGTAGATGAGTTCTTT 1420
                                                                                                                                                                                                                                                                                                                                    1505 GCACCTGAAGGTGAGGGCTGGCCTTTGACTACGCCGTTCTTAGTCTTCTCTTCTGAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                    686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                        626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/542-8906
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                                                                                                    Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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Pred. No. 4.4e-07;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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RESULT 19
US-09-165-522-11/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-130-616-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%;
Best Local Similarity 86.6%;
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 176
LENGTH: 2522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6943000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                   INFORMATION
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/165,522
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE:
                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
FEATURE:
                MOLECULE
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1501
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                                                      TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/060,995 FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                        LENGTH: 2522 base pairs
                                                                                                                               TELEX: 200154
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                                linear
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l, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alan
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Pred. No. 1.9e-06;
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US-09-949-016-17088
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; Sequence 17088, Application US/09949016
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Matches
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                                                                                                                                                                     Sequence 165, App
Patent No. 622185
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LENGTH: 48313
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Best Local Similarity
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    APPLICANT: McKay, Robert A.
APPLICANT: McKay, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
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LOCATION: (1)...(48313)
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les 71; Conserv
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SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                            Application US/09130616C
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ilarity 86.6%;
Conservative
ISPH-0318
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Pred. No. 1.9e-06;
0; Mismatches 11
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; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 2372
                                                                                                                                                                                                                                                                                   RESULT 23
US-09-130-616-173/c
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; ORGANISM: Homo sapiens
US-10-104-047-1930
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US-10-104-047-1930/c
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Sequence 173, Application US/09130616C
Patent No. 6221950
GENERAL INFORMATION:
APPLICANT: MCKAY, Robert A.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Moro, Pam
APPLICANT: Moro, Pam
APPLICANT: Nero, Pam
APPLICANT: Nero, Pam
APPLICANT: Nero, Pam
APPLICANT: Nero, Pam
APPLICANT: STILLE GRATCH, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
TILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
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Best Local (
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SEQ ID NO 165
LENGTH: 1408
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Best Local Similarity
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TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1382 GCACCTAAAGGAGAGGGCTGCCCCCGTATAACTCCATTCTTGGTTCTCCTCCCAAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
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Pred. No. 0.0041;
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; EARLIER FILING DATE: 1997-08-03; NUMBER OF SEQ ID NOS: 178; SEQ ID NO 173 ID NOS: 178; SEQ ID NO 173 ID NO 179; LENGTH: 1619; TYPE: DNA; ORGANISM: Homo sapiens US-09-130-616-173
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US-08-220-602B-17
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Query Match 6.0%;
Best Local Similarity 74.4%;
Matches 61; Conservative
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                       TELEFAX: (619) 678-509
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.,
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DERIJARD, BENOIT
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 25
                                                                                                                                                            TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
                                                                                               NAME/KEY:
                                                                                                                              CLONE: JNK2
                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: FI
STREET: 4225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                 1780 base pairs
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ANNING, LIN
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                                                                              CDS
59..1330
                                                                                                                                                                          linear
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                                                                                                                                                            DNA (genomic)
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; Pred. No. 0.01
0; Mismatches
 Score 48.4; DB 3;
Pred. No. 0.017;
0; Mismatches 21;
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     21;
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                                 Length 1780;
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Gaps

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FILE REFERENCE: REGEN1120-10
CURRENT APPLICATION NUMBER: US/09/861,098A
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 08/220,602
PRIOR FILING DATE: 1994-03-25
PRIOR FILING DATE: 1994-03-25
PRIOR APPLICATION NUMBER: US 08/094,533
PRIOR FILING DATE: 1993-07-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: US-09-861-012A-17
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Best Local Similarity
Matches 61; Conserv
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Patent No. 6846644
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                                                                                                                                                                               APPLICANT: KARIN, Michael
APPLICANT: DAVIS, Roger
APPLICANT: HIBI, Rosshiko
APPLICANT: LIN, Anning
APPLICANT: LIN, Anning
APPLICANT: DERIJARD, Benoit
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                  -09-861-098A-17/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KARIN, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (59)..(1330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1780
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LICANT: DERIJARD, Benoit
LE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
E REFERENCE: REGEN1120-12
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                                                                                                                                                                                                                                                                                                                                               Application US/09861098A
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HIBI, Masahiko
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Pred. No. 0.017;
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US-09-861-097-17/c
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Patent No. 6863888
GENERAL INFORMATION:
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LENGTH: 1780
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Best Local Similarity
                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 38.347

TELECOMMUNICATION INFORMATION: 07257/015001(PD3205)

TELEPHONE: (619) 678-5070

TELEPHAX: (619) 678-5099

MATION FOR SEC. 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MASAHIKO, HIBI
ANNING, LIN
DERIJARD, BENOIT
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,602
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.,
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, V CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,097
FILING DATE: 18-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE:
                                           FEATURE:
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ADDRESSEE: FISH &
STREET: 4225 Execu
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    NAME/KEY:
LOCATION:
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                                                              CLONE:
                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                             LENGTH: 1780 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
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                                                                JNK2
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    CDS
59..1330
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Pred. No. 0.017;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
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; NAME/KEY: CDS
; LOCATION: 59..1330
PCT-US94-12913A-17
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Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%;
Best Local Similarity 74.4%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application PC/TUS9412913A GENERAL INFORMATION:
                                                                                                                                                                                                                                               TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1780 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 9006/
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lin, Anning
APPLICANT: Derijard, Benoit
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: FD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/I
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION
                                                                                                                                             IMMEDIATE SOURCE:
CLONE: JNK2
                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                           NAME: LISA A. HAILE, PH.D. REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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   Conservative
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Davis, Roger
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                                                                                                                                                                                                                                                                                                                         (619) 455-5100
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                  6.0%;
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 Score 48.4; DB 7; Length 1780; Pred. No. 0.017; O; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48.4; DB 3;
Pred. No. 0.017;
0; Mismatches 21;
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RESULT 30
US-09-130-616-169/c
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                                                                                                 SEQ ID NO 169
LENGTH: 1782
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 169, Application US/09130616C Patent No. 6221850
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 16
                                                                                                                                                       APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
FULE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (59)..(1333)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L31951/Genbank
DATABASE ENTRY DATE: 1994-12-06
                                                                                                                                                                                                                                                                                                                                 APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: ISPH-0336
CURRENT APPLICATION NUMBER: US/09/209,668A
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
                                                                                                                                    NUMBER OF SEQ ID NOS: 178
                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 1782
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  6.0%;
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Pred. No. 0.01
0; Mismatches
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  Score 48.4;
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Length 1782;
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                                                                                                                                                                                                                                                                                                    Sequence 171, Application US/09130616C Patent No. 6221850
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Best Local
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SEQ ID NO 13750
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SEQ ID NO 171
            CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03 NUMBER OF SEQ ID NOS: 178
                                                                                                            APPLICANT: MCKAY, ROBERT A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Mero, Pam
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(132456)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                          126528 AACTTCCTTATATATCAATTCTGTAAAAGA 126499
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Similarity 71.1%;
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Pred. No. 0.055;
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0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 132456;
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                                                                                                                                                        AND METHODS
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENEANK
; CLONE: g1463128
US-09-023-655-953
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                                                  Matches
                                                                                                                                                                                                                                                                                         SOFTWARE: World Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERBWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REFERENCE/DOCKET NUMBER: 9A-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 953, Application US/09023655 Patent No. 6607879
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Cocks,
                                                                                                                                                                                                                                                               TELEFAX: (650) 845-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1392
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suman G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                              1392 base pairs
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                                                  Conservative
                                                                                                                                                 GENBANK
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                                                                                                                                                                                linear
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                                                                                                                                                                                               single
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                                                               5.8%;
77.0%;
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77.0%;
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                                                  Score 46.8; DB:
Pred. No. 0.041;
0; Mismatches
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                                                                               DB 3;
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                                                                               Length 1392;
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                                                   Indels
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; LENGTH: 1523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-172
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; ORGANISM: Human
US-09-949-016-5346
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/130,616C CURRENT FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 08/910,629 EARLIER FILING DATE: 1997-08-03 NUMBER OF SEQ ID NOS: 178 SEQ ID NO 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5346
LENGTH: 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5346, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
   Query Match
Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6221850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McKay, Robert A. APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1114 TAAATTAGCTCTTT 1101
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77.0%;
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77.0%;
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Score 46.8; DB Pred. No. 0.042; O; Mismatches
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                                    DB 3; Length 1523;
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Gaps
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RESULT 37
US-09-016-434-1437/c
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            Sequence 1437, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 57; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-UUN-1994
FILING DATE: 02-UUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
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CITY: E
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60 State Street
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77.0%;
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Pred. No. 0.043;
0; Mismatches 17,
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                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 53117
LENGTH: 601
                                                                                                                                                                                                                                                                                                                         Sequence 53117, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1437:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UPPLICATION STATE: HEREWITH CLASSIFICATION:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
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73.2%;
                                    Windows Version 4.0
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Pred. No. 0.044;
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; NAME/KEY: promoter;
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t.,
US-09-806-708B-22
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SEQ ID NO 22
LENGTH: 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Applica Patent No. 6784342 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
Matches 94; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants FILE REFERENCE: 4810-58741 CURRENT APPLICATION NUMBER: US/09/806,708B CURRENT FILING DATE: 2001-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
377
                                    415
                                                                                                                                                       257
                                                                                                                                                                                              295
                                                                                                                                                                                                                                  197
                                                                                                                                                                                                                                                                                                              137
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                                                                                                                                                                                                                                                                                                                                                                                                                              115 TNKWGKTGWRHRYWRWRAMBDTVDHHYVTAMNNAWTTMCMMDKDDKRTRWWWKKNNNATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 САБААТБААТБССАСАСТБААТАТСААААБААТАААТТААА ТСАТТАТААББАСАСА 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 AATACTTTTAAATTGTTTTTTAAACATTTTTACACATGAAAAATATCTTTTTCTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 ATTACTATTAAAATTATTATGAAAAAGTTTTTGTCCTGGATCATTACCATCAGAATAAT
                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 TTATAGTGAGAGCATAGGTCTTAGGAAAAAATATATTAGCATTAATAAGTAAATTGTCTC 77
                                                                                                                                                                                                                                                                                                          TAGATTCTGTGGCTAGCAAACGAAAATTTTCCAAGCTGACCTTAACCGGAGCCCATCTT 196
                                                                                                                                                                                                                                                                                                                                                                                        TCTTCAGGATTCATTACTATTAAAATTATTTATGAAAAAGTTTTTGTCCTGGATCATTAC 436
                                    WKMDMDWBGTYNNNNNGGRTYYGWTKNKKMWTYYKWKANNCKWRAWDHKTCTHNNTTWWK
                                                                                                                WTYKKARHBARWDWVWHSAWKKWHANAAHYSRKKWTBYKRKTMVNNNNGTTMWKRMWAWY 414
                                                                                                                                                 TGAGGGAAGAGGTAGCGGCTGAAAGGATTACTGAGCTCCACATTGACTTGATGGTCAAAA 316
                                                                                                                                                                                            WGWNRABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNNNNN 354
                                                                                                                                                                                                                                GGTAGATGTTTCAACTATTGTCACATCAACCTTGAGAAGAGTTCAAACACTAAGAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAATGACTTTATTCTTCATCTGGGCTAATACCTAACTAGTGCAAATACTTGAA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCATGTGATATTTGTCCATCTGCTCTTTAAGCAATGTTATGTTATTTCTTGCA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAACAGGATGTGACTAAAAACATTGACATATACAACATATGCATCAAAATAAGCAAATA
                                                                       GGGCATTATGGCTCTGAATTTTGATGAGGCACATTTACCCTTTAGCCCATGTTAACATTT 376
                                                                                                                                                                                                                                                                       KRKVRRWVRTRGRMRNYMVAWBTAHRRRYNNGWTBAMAYRRWTMNNNNNNAKAMCKRAKY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09806708E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 46; DB 3; Lilarity 11.0%; Pred. No. 0.061; Conservative 284; Mismatches 400;
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; ORGANISM: Artificial sequence ; FEATURE; NAME/KEY: promoter ; LOCATION: (1)..(1141) ; OTHER INFORMATION: consensus sequence of A.t., L.a., and US-09-806-708B-22
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US-09-806-708B-22/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DATE
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09806708B Patent No. 6784342 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR PILING DATE: 1999-08-04
NUMBER OF OF OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Regulation of Embryonic FILE REFERENCE: 4810-58741 CURRENT APPLICATION NUMBER: US/09/806,708B CURRENT FILING DATE: 2001-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                          1128
                                                                                                            1008
                                                                                                                                                                                 1068 RWCMRTYAMRTWYTRSNANWSCATKEMWWTMKWYATKYRTAWYAMWCAWRNNNMWCATNG 1009
311
                                948
                                                                     251
                                                                                                                                            191 CATCTTGGTAGATGTTTCAACTATTGTCACATCAACCTTGAGAAGAGTTCAAACACTAAG
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                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                      GTGTATTAGATTCTGTGGCTAGCAAACGAAAAATTTTCCAAGCTGACCTTAACCGGAGCC
                                                                   AATGAATGAGGGAAGAGGTAGCGGCTGAAAGGATTACTGAGCTCCACATTGACTTGATGG
                                                                                                        YAKSCATNNAMWYATTRWAAYAAAKWARWAGNNMRMYGAAAGNKWGCMAAMATMGBWWAD
                                                                                                                                                                                                                                                       TKTKTYKKANNNNNNNNGMGKDWNRMDATKWSATGTAWWTNHAKRGATMCWYWYWTGTNR 1069
                                                                                                                                                                                                                                                                                           TCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCACATTTACCCCTTTAGCCCATGTTA
                                  TAGKMCNNNNNWTTDVRRMAMKAKNNNNNNAYWTACYNRAATNNKMATHWMKWTHGAHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAAATTTATCCTTCATCCACAGGGAAATTCATTACTTAATGCCAAATA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAYTKYTTTNNNNTYRGVVTNTAARDGWANNNNNNNNNNNNNNGWSDMWVTWWAYANYGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGAGTGAGTACCTGA-AGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTC 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCARDDYYAASRWYAMANAKWYYYKBAANNAYYTHANNWWGCWNNATDTRRTMWKNNNN 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGCAACCCCTACACAAGGCCCAAGAAATTACACAAGTACTAGTTATTGGTTATTCAC
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                                                                                                                                                                                                                                                                                                                                Conservative 241;
                                                                                                                                                                                                                                                                                                                                               5.8%; Score 46; DB 3; 11.9%; Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                Mismatches
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                 밁
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                                                                                                                                                            ; FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (1)...(100877)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-13276
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US-09-949-016-13276
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PRIOR ETILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PAST-SEQ for Windows Versio:
SEQ ID NO 13276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13276,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                        Local
                 14071
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                                                                                        Conservative
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                                                                                    Score 46; DB pred. No. 0.2; 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
                                                        389 ATTACTATTAAAATTATTTATGAAAAAGTTTTTGTCCTGGATCATTACCATCAGAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 ATAGAAAACAAATTTATCCTTCATCCACAGGGAAATTCATTACTTAATGCCAAATAATTA
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AATACTTTTTAAATTGTTTTTTAAACATTTTTACACATGAAAAATATCTTTTTCTACAT 14130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTCTTCTGAATTCATTACTTCCTTGTAGATAAGTTCTGTAAGAAACAGCTGTGTTATT
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                                                                                                                                                                                               Length 100877;
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RESULT 43
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US-09-949-016-53116
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                                                                                                                                                                                                                                                                                                                           Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                                                            FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTMARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 53116
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Best Local (
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NAME/KEY: CDS
LOCATION: 235.
-09-621-976-2813
                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001307
                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 168, Application US/09130616C
PATENT NO. 6221850
GENERAL INFORMATION:
APPLICANT: MCKAy, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nonia, Brett
APPLICANT: Nonia, Brett
APPLICANT: Nonia, Brett
APPLICANT: Nonia, Pam
APPLICANT: Nonia, Pam
APPLICANT: Nonia, William A.
APPLICANT: OBARTHO: WILLIAM A.
APPLICANTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: 15PH-0318
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Best Local S
Matches 59
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SEQ ID NO 168
                                                                                                                                   Query Match
Best Local Similarity
Matches 60; Conserv
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                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE:
                                                                                                                                                                                                                       LENGTH: 1349
TYPE: DNA
ORGANISM: Homo sapiens
1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 АСАСТБААТАТСААЛАБАЛАТАЛААСТАЛАЛТСАТТАТАЛББАСАСЛАССАТБТБАТАТТ
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59; Conservative
                       ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                     TAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATCCACAGG
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ATAACTTCCTTATATATCAATTCTTT 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYKKGSTYWTMKCTCATWCYWYWKYWKRMWSKTCWSGSRGGYMTSYTSTRSYSMYWASWM
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                                                                   GCACCTAAAGGAGAGGGCTGCCCCCGTATAACTCCA1
                                                                                                                                   5.5%;
nilarity 69.8%;
Conservative
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17.7%;
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                                                                                                                                   Score 44.4; DB
Pred. No. 0.16;
D; Mismatches
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                                                                                                                                                                       Length 1349;
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RESULT 45
US-09-130-616-166/c
y Sequence 166, Application
patent No. 6221850
GENERAL INFORMATION:

US/09130616C

APPLICANT: McKay, Robert

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.474
FILING DATE: HERFWITM:
CLASSITETING PRICE PROFESSIONAL PRICE PRICE PRICE PROFESSIONAL PRICE PRICE PROFESSIONAL PRICE PRICE PROFESSIONAL PRICE PRICE PROFESSIONAL PRO
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LENGTH: 1365
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: GOMBOGITTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-016-434-1139/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gearde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
                                                                                                 TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 113
SEQUENCE CHARACTERISTICS:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING TITLE OF INVENTION: PATHWAY GENE EXPRESSION
STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                ENGTH:
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ucleic acid
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Pred. No. 0.16;
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; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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US-09-621-976-2813
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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Best Local
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CURRENT FILING DATE: 2000-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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LIBRARY: GENBANK
CLONE: g1463130
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Local Similarity 69.8%;
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385
                               413
                                                                    325
                                                                                                                                                                                                              205
                                                                                                                                                                         293 TCCACATTGACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCACATTT
                                                                                                                                                                                                                                                233 AAGAGTTCAAACACTAAGAATGAATGAGGGAAGAGGTAGCGGCTGAAAGGATTACTGAGC
                                                                                                                                                                                                                                                                                   145 KRWKKAWTTWWWKKTYYWAATRYWWMMCWTKRWRASWWYCWWWGKARKWSTWRKSRSYAS
                                                                                                                                                                                                                                                                                                                                                                                          123 GCACAATTGTGTATTAGATTCTGTGGCTAGCAAACGAAAAATTTTCCAAGCTGACCTTAA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                       CCGGAGCCCATCTTGGTAGATGTTTCA-----ACTATTGTCACATCAACCTTGAG
                                                                                                                                                                                                                                                                                                                                                        GYMWMWYWGWRRSYMAMWTRTWTGYAYYRSMMYWWRYRCWKKKAYYRKTTCYSSKGWTWW 144
ACAATTCTTGTACTTTAGCA 404
                                                                    RASMWWRRWYYTMMKKWWKYAWARAAWRWWAMWWAWRRACAAAATATAATTATTATGGT
                                                                                                      WMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYMWKRWWWCWARMYRYSTGT
                                                                                                                                                                                                            ARSAKRCCYSCSWGAMSWKYMWRWRWRGWATGAGMKAWRASCMMRRKYAGKSKTSYKSM
                               AAAGTTTTTGTCCTGGATCA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.3%; Score 42.4; DB nilarity 16.6%; Pred. No. 0.45; Conservative 153; Mismatches 1
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; ORGANISM: Homo sapiens
US-09-130-616-167
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US-09-130-616-167/c
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/209,668A
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09209668A
Patent No. 6114517
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Best Local Similarity
Matches 57; Conserv
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LENGTH: 1311
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                                                                           Matches
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                                                                                                                                                          -09-209-668-14
                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (19)..(1173)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L26318/Genbank
DATABASE ENTRY DATE: 1994-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Monia, Brett P.

APPLICANT: Xu, Xiaoxing S.

TITLE OF INVENTION: AUTHODS OF MODULATING TUMOR NECROSIS FACTOR

TITLE OF INVENTION: Alpha-INDUCED EXPRESSION OF CELL ADHESION M
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: FOR THE MODULATION OF JNK
FILE REFERENCE: ISPH-0318
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APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-209-668-14/c
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                        ENGTH: 1418
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1156 CTAAAGGAGAGGGCTGCCCCCGTATAACTCCATTCTTGGTTCTCTCCTCCAAGTCCATAA 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1156 CTARAGGAGAGGGCTGCCCCCGTATAACTCCATTCTTGGTTCTCCTCCTCCAAGTCCATAA 1097
                    630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 CTTCCTTGTAGATAAGTTCTGT 711
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; ORGANISM: Homo sapiens
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Search completed: July 19, 2006, 20:14:12 Job time: 207 secs
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Best Local Similarity 69.5%;
Matches 57; Conservative
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Patent No. 622185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE COMPOSITIONS AND METHODS TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
BARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
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Maximum Match 100%
Listing first 100
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   Published_Applications
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Sequence 2, Appli
Sequence 683711,
Sequence 4942, Ap
Sequence 4944, A
Sequence 44644, A
Sequence 44644, A
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Sequence 175291,
Sequence 23, Appl
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Sequence 1820, Ap
Sequence 17, Appli
Sequence 27, Appli
Sequence 27,
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Sequence 2. Application US/10723681

Publication No. US20050192239A1

GENERAL INFORMATION:

APPLICANT: ROTH, RICHARD B.

APPLICANT: NELSON, MATTHEW ROBERTS

APPLICANT: REMAUN, ANDREAS

APPLICANT: REMELAND, RIKARD

TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND

TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND

TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND

TITLE OF INVENTION UNMERN'S THEREOF

CURRENT APPLICATION NUMBER: US/10/723,681.

CURRENT APPLICATION NUMBER: US/60/429,136

PRIOR APPLICATION NUMBER: US 60/429,136

PRIOR APPLICATION NUMBER: US 60/429,234

PRIOR APPLICATION NUMBER: US 60/490,234

PRIOR FILING DATE: 2003-07-24

NUMBER OF SEQ ID NOS: 835

SOFTWARE: Patentin version 3.2

LENGTH: 76500
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Best Local Similarity 99.9%;
Matches 799; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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              GCCCATGTTAACATTTTCTTCAGGATTCATTACTATTAAAATTTATTATGAAAAAGTTTT
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Sequence 75, Appl
Sequence 76, Appl
Sequence 758673,
Sequence 758673,
Sequence 396, App
Sequence 396, App
Sequence 758672,
Sequence 376, App
Sequence 377, App
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US-10-857780-2

US-10-857780-2

US-10-857780-2

Sequence 2, Application US/10857780

Publication No. US20050272043A1

GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: KAMMERER. STEFAN M.
APPLICANT: KAMMERER. STEFAN M.
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RIS
TITLE OF INVENTION: METHODS FOR IDENTIFYING RIS
TITLE OF INVENTION UMMBER: US/10/857,780

CURRENT FILING DATE: 2003-01-25

PRIOR APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-01-25

UMMBER OF SEQ ID NOS: 4962

SOFTWARE: PatentIn version 3.2

FILING THE SOURTH STANDARD SERVICE SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                       ; LENGTH: 110950
; TYPE: DNA
; ORGANISM: Homo s
US-10-857-780-2
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Best Local Similarity
Matches 799; Conserv
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Pred. No. 2.6e-178;
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FILE OF INVENTION: NUCLEUCIUG FOLYNWALPHILENS
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 683710
LENGTH: 2669
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US-09-925-065A-683710/c
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
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   RESULT 4
US-09-25-065A-683711/c
Sequence 683711, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
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US-09-925-065A-683710
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Matches 798;
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Pred. No. 1.2e-178;
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-01-05-09
NUMBER OF SEG ID NOS: 957086
SOPTWARE: FASTSEQ for Windows Version 4.0
SEG ID NO 683711
LENGTH: 2669
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Best Local Similarity 99.8
Matches 798; Conservative
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Pred. No. 1.2e-178;
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WESULT 5
US-09-925-065A-683712/c
Sequence 683712, Application US/09925065A
Publication No. US20040181.048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
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Best Local Similarity 99.8
Matches 798; Conservative
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TYPE: DNA
ORGANISM:
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Pred. No. 1.2e-178;
0; Mismatches 2;
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US-09-925-065A-683710/c
; Sequence 683710, Application US/09925065A
; Publication No. US20050228172A9
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CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PRILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR APPLICATION NUMBER: US 60/289,846
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 683710
LENGTH: 2669
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Best Local Similarity
Matches 798; Conserv
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ORGANISM: Homo sapiens
-09-925-065A-683710
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Pred. No. 1.2e-178;
0; Mismatches 2;
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Sequence 683711, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human General Reference: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2000-10-1-16

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086
US-09-925-065A-683711
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                                                                                                                      SOFTWARE: FastSEQ for Windows SEQ ID NO 683711
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99.6%;

Score 796.8;

DB 5;

Length 2669;

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RESULT 8
US-09-925-065A-683712/c
Sequence 683712, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human General Reference: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 683712
LENGTH: 2669
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Pred. No. 1.2e-178;
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FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PACENTIN VERSION 3.2
LENGTH: 823
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Best Local Similarity 99.8%;
Matches 464; Conservative
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ORGANISM: Homo sapiens
-10-857-780-4942
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APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: THEREOF
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APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFA
APPLICANT: NELSON, MATTHEW
APPLICANT: RENELAND, RIKAR
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Pred. No. 1.3e-99;
0; Mismatches 1
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PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-10-24
PRIOR FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: Patentin version 3.2
SEQ ID NO 4943
LENGTH: 823
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Best Local Similarity 99.8%;
Matches 464; Conservative
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APPLICANT: ROTH, RICHARD B.
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APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILLING DATE: 2004-05-28
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APPLICANT: KAMMERER, STEFAN M.
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CACAGGGAAATTCATTACTTAATGCCAAATAATTACGTTTTGATG
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Pred. No. 1.3e-99;
0; Mismatches 1;
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RESULT 11
US-09-925-065A-44644/c
US-09-925-065A, Application US/09925065A
; Sequence 44644, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single
 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human

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RESULT 12
US-09-925-065A-44644/c
; Sequence 44644, Application US/09925065A
; Publication No. US20050228172A9
; Publication No. US20050228172A9
; GENERAL INFORMATION;
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of TITLE OF INVENTION: Nucleotide Polymorphisms in t FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR APPLICATION NUMBER: US 60/252,147
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-24
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
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Best Local Similarity 99.8%;
Matches 457; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44644
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ORGANISM: Homo sapiens
-09-925-065A-44644
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Pred. No. 5.3e-98;
0; Mismatches 1
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LENGTH: 572 TYPE: DNA ORGANISM: Homo sapien -10-301-480-145882

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Single Nucleotide Polymorphisms

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US-10-301-480-145882/c
US-10-301-480-145882, Application US/10301480
; Sequence 145882, Application US/10301480
; Publication No. US/20060057564A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of TITLE OF INVENTION: Identifiction and Mapping of TITLE OF INVENTION: Identifiction and Mapping of CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FASCSEQ for Windows Version 4.0
; SEQ ID NO 145882
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 44644
LENGTH: 572
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GENERAL INFORMATION:

APPLICANT: WANG, David G.

TITLE OF INVENTION: identifiction and Mapping of TITLE OF INVENTION: in the Human Genome FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FRASTSEQ for Windows Version 4.0

SEQ. ID NO 759291

LENGTH: 572
                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-759291
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US-10-301-480-759291/c
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Best Local Simi
Matches 457;
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 759291, Application US/10301480 Publication No. US20060057564A1
                                                                                                                                              Best Local Sim Matches 457;
                                   512
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ilarity 99.8%;
Conservative
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99.8%;
                                                                                                                                             Score 456.4; DB 12; Pred. No. 5.3e-98; 0; Mismatches 1;
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Pred. No. 5.3e-98;
0; Mismatches 1
                                                                                                                                                                         DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                     of Single Nucleotide Polymorphisms
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                                                                                                                                                                        Length 572;
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RESULT 16
US-09-165-522-1/c
; Sequence 1, Application US/09165522
; Publication No. US20030023990A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; Flavell, Richard A.
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                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: homo sapiens US-09-909-650A-23
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Best Local S
Matches 84
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SEQ ID NO 23
LENGTH: 1422
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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 29
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APPLICANT: Aventis Pharmaceuticals Inc.
APPLICANT: Fournier, Alain
APPLICANT: Maury, Isabelle
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
APPLICANT: Zhou-Liu, Qing
APPLICANT: Desanlis-Cremond, Francine
TITLE OF INVENTION: New Polypeptides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 CTGTCCTTTTÄCTÄCÄCCATTTTTÄGTCTTTTCTTCTGAATTCÄTTÄCTTCCTTGTÄGÄT
                           GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTC
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GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                                                                                         Score 82.8; DB 3;
Pred. No. 5.5e-09;
                                                                                                                                           Length 1422;
                                                                                                 Indels
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                                                                                            Gaps
    1224
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Sequence 952, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                          RESULT 17
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Matches 84; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                      APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 68...1459
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAC: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/165,522 FILING DATE: 02-Oct-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                    1323 GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                         626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
                                                                                                                                                                                                                                                                                              ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
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                                                                                             THE DETECTION OF BLOOD CELL
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                                                                                                                                                                                                                                                                                                                                                                    TTC 1264
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RESULT 18
US-10-343-710-56/c
                                                                  US-10-343-710-56
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                                                                             SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/103 Publication No. US20040087478A1 GENERAL INFORMATION:
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Query Match
Best Local Similarity
                                                                                                                                                                                          TITLE OF INVENTION: SCREENING METHOD FILE REFERENCE: 029310.52022US CURRENT EPPLICATION NUMBER: US/10/343,710 CURRENT FILING DATE: 2003-09-17 PRIOR APPLICATION NUMBER: PCT/EP01/09011 PRIOR FILING DATE: 2001-08-03 NUMBER OF SEQ ID NOS: 157
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-41.
INFORMATION FOR SEQ ID NO: 952:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION UNMBER: «Unknown»
FILING DATE: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: PA-0001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10500 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 10.3%;
Local Similarity 97.7%;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
FILING DATE: 14-Aug-2003
CLASSIFICATION: UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1263 ATTACTTCCTTGTAGATAAGTTCTTT 1238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                 WETZELS, Ingrid
WNENDT, Stephan
WEIHE, E.
SCHAEFER, M., K.-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACTTCCTTGTAGATAAGTTCTGT 711
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CLONE: 91463124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10343710
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  10.3%;
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  Score 82.8; DB 8; Pred. No. 5.6e-09;
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Pred. No. 5.6e-09;
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                      Length 1505;
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                                                          Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 1036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equence 1, Application US/11180044 ublication No. US20060035303A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                              TELEX: 200154
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                     MOLECULE TYPE:
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ADDRESSEE: Fish & Richardson P.C.
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APPLICANT: Yang, Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                               LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                      TOPOLOGY:
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                GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTGAAATTC 1264
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                                                            Conservative
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Rakic, Pasko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whitmarsh, Alan
                                                                                                                                      Coding Sequence 68...1459
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                                                                         Score 82.8; DB 16
Pred. No. 5.6e-09;
                                                            Mismatches
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                                                                                       DB 16;
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                                                                                       Length 1505;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-817-10
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US-11-127-817-10/c
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LENGTH: 2211
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Best Local Similarity
Matches 84; Conserv
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TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                     Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS
NUMBER OF SEQUENCES: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Davis, Roger J.
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                  CITY: Boston
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10. US20050287519A1
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Whitmarsh, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flavell
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97.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richard A.
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Pred. No. 6.7e-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.3%;
Best Local Similarity 97.7%;
PILING DATE: 12-JULY-2005

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-OCC 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/0050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USB NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/11/180,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1419
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis, Roger J.
Flavell, Richard
Rakic, Pasko
Whitmarsh, Alan
Kuan, Chia-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                     IBM Compatible
SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richard A
                        10363/005001
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Pred. No. 6.9e-09;
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SEQ ID NO 34
LENGTH: 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/10765700 Publication No. US20050130171A1
                                                                                                                                    Matches
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/10/765,700
CURRENT FILING DATE: 2004-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIORT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    NAME/KEY: unsure LOCATION: 2024
                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Incyte ID No: 413797.5
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2367 base pairs
1735 ATTACTTCCTTGTAGATAAGTTCTTT 1710
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                                 989
                                                                                    626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC
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                              ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                 GCACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 1736
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97.7%;
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                                                                                                                                                 Score 82.8; DB 10
Pred. No. 7.3e-09;
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Pred. No. 6.9e-09;
                                                                                                                                    Mismatches
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                                                                                                                                                                10;
                                                                                                                                                                Length 2677;
                                                                                                                                    Indels
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                                                                                                                                  Gaps
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US-11-127-817-11/c

Sequence 11, Application US/11127817 Publication No. US20050287519A1

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel

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                                                                                                                                                                                                                                    ; LOCATION: (373)..(453)

OTHER INFORMATION: 100% homologous to Mus musculus JNK3, accession number;
OTHER INFORMATION: AB005665, Smith-Waterman Score=136.
US-10-450-763-29386
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; ORGANISM: Homo sapiens
US-11-127-817-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 97.7%; Pred. No. 7.3e-09; Matches 84; Conservative 0: Migmathic
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Custom
SEQ ID NO 29386
LENGTH: 972
                                                                                                                                                     Matches 81;
                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -10-450-763-29386/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 60/603,948
PRIOR FILING DATE: 2004-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 534
SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Laenen, Wendy
TITLE OF INVERVION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                              NAME/KEY: SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2698
                                                                                                                                                                          Local Similarity
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  393
                                       688 TACTTCCTTGTAGATAAGTTCT 709
                                                                            453
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                                                                                                                 628 ACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCAT 687
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                                                                                                                                                          Conservative
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                                                                                                                                                                          10.1%;
                                                                                                                                                        <u>.</u>
                                                                                                                                                                    Score 80.4; DB 10
Pred. No. 1.7e-08;
                                                                                                                                                        Mismatches
                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYPEPTIDES
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                                                                                                                                                                                               972;
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                                                                                                                                                        Gaps
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US-10-450-763-11488
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US-10-450-763-11488/c
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US-10-450-763-2768/c
                                                                                                                                                                                        SOFTWARE: Custo
SEQ ID NO 11488
LENGTH: 1111
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CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11488, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
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SOFTMARE: CUSTOM
SEQ ID NO 2768

LENGTH: 999

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (373)..(453)
OTHER INFORMATION: 100% homologous to Mus musculus JNK3,accession number
OTHER INFORMATION: AB005665,Smith-Waterman Score=136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 790CIP3/US
                         LOCATION: (25)..(1452)
OTHER INFORMATION: 81% homologous to Homo sapiens putative p150,accession number
OTHER INFORMATION: U93572,Smith-Waterman Score=1883.
                                                                                               NAME/KEY: SIMILAR
                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                             Custom
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Matches

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RESULT 28

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APPLICANT: Zhou-Liu, Qing
APPLICANT: Desanlis-Cremond, Francine
APPLICANT: Desanlis-Cremond, Francine
TITLE OF INVENTION: New Polypeptides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: POT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                  US-09-165-522-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application UP Patent No. US20020165386A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Aventis Pharmaceuticals Inc APPLICANT: Fournier, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1306
                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                             Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                          AL INFORMATION:
AL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Playell, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1219 CTTCCTTGTAGATAAGTTCTTT 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1279 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1220
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COUNTRY: USA
ZIP: 02110-2804
                                     STATE: MA
                                                         CITY: Boston
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                                                                                                                                                                                                                                                    Rakic, Pasko
                                                                                                                                                                                                                                  Whitmarsh, Alan
                                                                                                                                                                                                     Kuan, Chia-Yi
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Pred. No. 2e-08;
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APPLICANT: GILLEN, Clemens
APPLICANT: WIETZELG, Ingrid
APPLICANT: WRENDT, Stephan
APPLICANT: WEIHE, E.
APPLICANT: SCHAFFER, M., K.-H.
APPLICANT: SCHAFFER, M., K.-H.
TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 023310.52022US
                                                                                                 ; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-343-710-54
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               Query Match 10.1%; Score 80.4; DB 8; Best Local Similarity 98.8%; Pred. No. 2.2e-08; Matches 81; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54, Application US/10343710 Publication No. US20040087478A1
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Best Local Similarity
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/343,710 CURRENT FILING DATE: 2003-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: FABSESC for WINDOWS Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-0cc-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
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US-11-180-044-4
                                                                                         Query Match
Best Local S
Matches 81
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NAMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/11/180,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                   NAME: Fasse, J. Peter REGISTRATION NUMBER
                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                          : YEOTOGA
                                                                                                                                                                                                                     STRANDEDNESS:
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                                       TY: Boston
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690 CTTCCTTGTAGATAAGTTCTGT 711
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                                                                                          81;
                                                                                                      Similarity
                                                                                                                                                                                                                     nucleic acid
EDNESS: double
                                                              CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 Franklin Street
                                                                                                                                                                                                                                            1773 base pairs
                                                                                                                                                                                                                                                                                                617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Yang, Di
                                                                                          Conservative
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Flavell, Richard A.
                                                                                                                                                       Coding Sequence 92...1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
SYSTEM: Windows 95
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Fish & Richardson P.C.
                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                 J. Peter
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                                                                                                   10.1%;
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                                                                                       Score 80.4; D
Pred. No. 2.2e
0; Mismatches
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                                                                                                   .2e-08;
                                                                                                                  DB 16;
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US-09-771-161A-87/c
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                                                                                                               SOFTWARE: Pa
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIMILAR
                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   889
                                                                                                     2131
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                                                                                                                            PatentIn
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Sequence 87, Application US/09771161A Patent No. US20020110811A1
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Publication No. US20050196754A1
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS Of PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-10
PRIOR APPLICATION UNMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hyseq, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 790CIP3/US
NAME/KEY: -
LOCATION: (1)..(2131)
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1563)..(1688)
OTHER INFORMATION: 80% homologous to Homo sapiens Human secreted protein, SEQ ID
OTHER INFORMATION: NO: 7131,accession number G03050,Smith-Waterman Score=173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1283 CTTCCTTGTAGATAAGTTCTTT 1262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628 ACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTT
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                                                                                                                                                                                                                       version 3.0
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Pred. No. 2.3e-08;
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1165

690

Matches

US-11-127-817-12/c

RESULT 34

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-817-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/111 Publication No. US20050287519A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad
APPLICANT: Laenen, Wendy
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1198 CTTCCTTGTAGATAAGTTCTTT 1177
                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                            Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                         APPLICANT: Davis, Roger J. Flavell, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1258 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1199
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                                                               STATE: MA
                                                                                                         STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/11127817
                                                                                 TY: Boston
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                                                                                                                                                                                                                                                                       Rakic, Pasko
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Pred. No. 2.5e-08;
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Pred. No. 2.4e-08;
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, Sequence 7, Application US/09165522
; Publication No. US20030023990A1
; GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 6:
                                                         COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast52Q for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATA: 02-Oct-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 60/060,995 FILING DATE: 03-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/165,522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: MA
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rakic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuan, Chia-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.1%; Score 80.4; DB 3; 98.8%; Pred. No. 2.6e-08; vative 0; Mismatches 1;
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Matches

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US-09-165-522-6/c

GENERAL INFORMATION

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RESULT 38
US-10-466-162-5/c
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; LOCATION: 224...1489
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-165-522-7
                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: misc feat
; OTHER INFORMATION:
US-10-305-720-1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ś
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Sequence 5, Application US/10466162 Publication No. US20050170343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1389, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PERL Program
EQ ID NO 1389
LENGTH: 2372
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                               1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1475 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 1416
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                                                                                                                                                                                630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTTCTGAATTCATTA 689
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                                                                                                                                                                                                                              81;
                                                                                                                  CTTCCTTGTAGATAAGTTCTGT 711
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TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/542-8906
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                         GenBank ID No. US20040010136A1 g468150
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Pred. No. 2.6e
0; Mismatches
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Pred. No. 2.6e-08;
0; Mismatches 1
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; ORGANISM: Homo sapiens
US-10-466-162-5
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                                                            NUMBER OF SEQ ID NOS: 835
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
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SEQ ID NO 5
LENGTH: 2372
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Publication No. US20050192239A1
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Best Local Similarity
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                                                                                                   FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/723,681
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: US 60/429,136
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/490,234
PRIOR APPLICATION NUMBER: US 60/490,234
PRIOR FILING DATE: 2003-07-24
NUMBER OF SEQ ID NOS: 835
                                                                                                                                                                                                                                                                    APPLICANT: KAMMERER, STEFAN M.
APPLICANT: RENELAND, RIKARD
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND
TITLE OF INVENTION: TREATMENTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NOTH,
APPLICANT: NELSC
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PRIOR APPLICATION NUMBER: US 60/261,694
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,532
PRIOR FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/466,162
CURRENT FILING DATE: 2003-07-11
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-01-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US FILING DATE: 2001-01-12
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APPLICATION NUMBER: US
FILING DATE: 2001-01-12
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NELSON, MATTHEW ROBERTS
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RESULT 41
US-11-127-817-9/c
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Best Local Similarity
                                                                                                                                                                                    Sequence 9, Application US/11127817 Publication No. US20050287519A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR PILING DATE: 2003-07-24
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
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NUMBER OF SEQ ID NOS: 4962
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APPLICANT: HOYAL-WRIGHTSON, CAROLIN R.
TITLE OF INVENTION: WETHOUS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: THEREOF
                                                                                                                                             APPLICANT: Merchiers, Pascal G. APPLICANT: Hoffmann, Marcel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/525,239
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAMMERER, STEFAN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RICHARD B.
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Pred. No. 2.6e-08;
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Pred. No. 2
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US-11-180-044-6/c
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SEQ ID NO 9
LENGTH: 2372
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Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                  APPLICATION UNMBER: US/11/180,044
FILING DATE: 12-UULY-2005
PRIOR APPLICATION DATA:
US/09/165,522
PRIOR APPLICATION UNMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/060,995
PRIOR APPLICATION UNMBER: 60/060,995
PRIOR APPLICATION UNMBER: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/0050
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
                                                                                                              NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FeatSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kuan, Chi
APPLICANT: Yang, Di
TITLE OF INVENTION:
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                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flavell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                            double
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Chia-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roger J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JNK3 MODULATORS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60/603,948
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RESULT 43
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                Query Match
Best Local :
                                                                                                                                                                               INCLEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 bacc
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                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                         NAME: FASSE, J. PELE:
NAME: FASSE, J. PELE:
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 1036:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 17/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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Local Similarity 98. hes 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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                                                                               OCATION:
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                                                                                                                                                                                         2372 base pairs
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225 Franklin Street
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Whitmarsh, Alan
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Yang, Di
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                                                                               Coding Sequence 224...1489
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                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                DNA
10.1%; Score 80.4; I
98.8%; Pred. No. 2.60
ative 0; Mismatches
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Pred. No. 2.6e-08;
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               6e-08;
                            DB 16; Length 2372;
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Sequence 8, Application US/09776167A
Patent No. US20020058243A1
GENERAL INFORMATION:
APPLICANT: Jarnigan, Kurt
APPLICANT: Greene, Amy
TITLE OF INVENTION RAPID, PARALLEL IDENTIFICATION OF CELL LINES
FILE REFERENCE: 0024.US
CURRENT APPLICATION NUMBER: US/09/776,167A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: USSN 60/179,893
PRIOR APPLICATION NUMBER: USSN 60/179,893
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
US-09-776-167A-8
                                                                                                                                                                                                                                                                                                                               RESULT 45
US-09-776-167A-8/c
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; LOCATION: 1770-1816
; OTHER INFORMATION: a,
US-10-765-700-33
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Best Local Similarity
Matches 81; Conserv
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LENGTH: 2982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33; Application US/10765700 Publication No. US20050130171A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/765,700
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIORT FILING DATE: 2000-05-05
   TYPE: DNA
ORGANISM: pFastFind-JNK3
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SOFTWARE: PERL Program
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 413797.7
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                                                  ENGTH: 8750
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Query Match

10.1%;

Score 80.4;

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Length 8750;

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Best Local Similarity
""" hes 74; Conserv?
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; ORGANISM: Rattus norvegicus
US-11-136-527-4334
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US-11-136-527-4334/c
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 4334
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 600
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASESEQ for Windows Version 2.0b
CURRENT APPLICATION NUMBER: US/09/165,522
                                                                                                                                                                                                               Whitmarsh, Alan
Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Davis, Roger J. Flavell, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                             STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTACTTCCTTGTAGATGAGTTCTTT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACCTGAAGGTGAGGGCTGGCCTTTGACTACGCCGTTCTTAGTCTTCTTCTTGAGTTC
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                                                                                                                           COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 2.4e-05;
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0; Mismatches 1;
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TYPE: DNA
GRGANISM: Rattus norvegicus
US-10-343-710-60
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US-10-343-710-60/c
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                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingric
APPLICANT: WNENDT, Stephan
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WEIHE, E.
APPLICANT: SCHAEFER, M., K.-H.
TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                Local Similarity
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                           1505 GCACCTGAAGGTGAGGGCTGGCCTTTGACTACGCCGTTCTTAGTCTTCTTCTTCTGAGTTC 1446
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       1445 ATTACTTCCTTGTAGATGAGTTCTTT 1420
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                                                                                                           626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685
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WNENDT, Stephan
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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llarity 86.0%;
Conservative
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Pred. No. 4e-0
0; Mismatches
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4e-05;
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US-11-136-527-238/c ; Sequence 238, Application US/11136527 ; Publication No. US20050287570A1
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                                                          RESULT 50
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SOPTWARE: FABCESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-UULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/99/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: 32,983
APPLICATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TRLECOMMUNICATION: NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION: NORMATION:
TELEPHONE: 617/542-5970
TELEPHONE: 617/542-6906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENUTH: 1075 base Daire
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Best Local Similarity
Matches 74; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 N
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPONERATING SYSTEM:
SOFTWARE: FASTSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                  1505 GCACCTGAAGGTGAGGGCTTGGCCTTTGACTACGCCGTTCTTAGTCTTCTTCTTGAGTTC 1446
                                                                                                                                              686 ATTACTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                         74; Conservative
                                                                                                                     ATTACTTCCTTGTAGATGAGTTCTTT 1420
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Flavell, Richard A.
Rakic, Pasko
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Search completed: July 19, 2006, 23:05:29
Job time : 1478 secs
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                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 238
LENGTH: 1980
                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 74; Conserv
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Rattus norvegicus
                                                                          1445
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                                                                          ATTACTTCCTTGTAGATGAGTTCTTT 1420
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Pred. No. 4e-05;
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Result
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Maximum
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Perfect score:
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and is derived by a
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4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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S-11-266-748A-57178

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S-11-266-748A-31578

S-11-266-748A-382414

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S-11-266-748A-43999

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S-11-266-748A-122015
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S-11-266-748A-292324
S-11-266-748A-343753
S-11-266-748A-403979
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 -11-283-329-231
-11-266-748A-182241
-11-266-748A-242782
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 Sequence
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2403973,
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US-11-266-748A-223967/c
                                                                                                                                                                              Sequence 292324, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR APPLICATION NUMBER: EP 04105507.0
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PRICING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105484.2
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US-11-266-748A-343753
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; Publication No. US20060134663A1
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US-11-266-748A-292324
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SOFTWARE: PatentIn version 3
SEQ ID NO 343753
Query Match
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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APPLICANT: Johnston, P
APPLICANT: Mulligan, K
                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
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NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: US 60/700,293
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
                                                                                                                                    LENGTH: 1000
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  Score 82.8;
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  DB 8;
  Length 1000;
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RESULT 4
US-11-266-748A-403979/c
; Sequence 403979, Application US/11266748A
; Publication No. US20060134663A1
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Best Local S
                                                                                                        GENERAL INFORMATION:
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
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NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: EP 04105479.2
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105483.4
FILING DATE: 2004-11-03
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Mulligan, Karl
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Pred. No. 1.3e-10;
0; Mismatches 2;
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PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 475025
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US-11-266-748A-403980
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
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PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105483.4
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97.7%;
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Pred. No. 1.3e-10;
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US-11-266-748A-475025
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PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR PRIOR PRIOR PRIOR NUMBER: EP 04105484.2
PRIOR PRIOR FILLING DATE: 2004-11-03
                                                Sequence 57178, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version EQ ID NO 475026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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APPLICANT: Johnston, I
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                     989
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Harkin, Paul
Johnston, Patrick
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Mulligan, Karl
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97.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 82.8; DB 8; Length 1000; Pred. No. 1.3e-10;
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Pred. No. 1.3e-10;
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TITLE OF INVENTION: Transcriptome Microarray Techn
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION UMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 0410548.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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US-11-266-748A-57178
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1263 ATTACTTCCTTGTAGATAAGTTCTTT 1238
                                                                      686 ATTACTTCCTTGTAGATAAGTTCTGT 711
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97.7%;
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Pred. No. 1.6e-10
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US-11-266-748A-31164/c
Sequence 31164, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Horkin, Paul
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105402.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2005-07-18

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; ORGANISM: Homo Sapiens
US-11-266-748A-31164
                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 349578
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Best Local
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF CEO TO MOO 1000-07-07
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CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03
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PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                             NAME/KEY: misc feature LOCATION: (1979)..(2028) OTHER INFORMATION: n is a,
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                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                     ENGTH: 3232
                                                                                          Local Similarity
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APPLICATION NUMBER: EP 04105484.2
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Mulligan, Karl
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US-11-266-748A-432957, Application US/11266748A; Sequence 432957, Application US/11266748A; Publication No. US20060134663A1; GENERAL INFORMATION:
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, NAME/KEY: misc_feature
, LOCATION: (1979)..(2028)
, OTHER INFORMATION: n is a,
US-11-266-748A-382414
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Best Local Similarity
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                                        APPLICANT: Harkin, Paul
APPLICANT: Johnston, P
APPLICANT: Mulligan, K
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
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CURRENT APPLICATION NUMBER: US/11/266,748A
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LOCATION: (161)..(201)
OTHER_INFORMATION: n is
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                                      Johnston, Patrick
Mulligan, Karl
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Mulligan, Karl
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Transcriptome Microarray Technology and Methods of Using the Same
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Pred. No. 1.
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FILE REFERENCE: 55815-0102 (319189)

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APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.7
PRIOR APPLICATION NUMBER: EP 04105485.6
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; LCCATION: (3032)..(3072)
; OTHER INFORMATION: n is a, c,
US-11-266-748A-432957
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Best Local :
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: EP 04105482.6
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CURRENT FILING DATE: 2005-11-03
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LOCATION: (1205)..(1254)
OTHER INFORMATION: n is a,
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
                                                APPLICATION NUMBER: EP 04105485.9
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APPLICATION NUMBER: EP 04105507.0
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Pred. No. 1.8e-10;
0; Mismatches 2
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Best Local Similarity
Matches 62; Conserve
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; ORGANISM: Homo Sapiens
US-11-266-748A-403999
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; Sequence 403999, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-46908
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SEQ ID NO 46908
LENGTH: 801
                                                                                                                                             Matches
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CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION UNUBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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PRIOR APPLICATION NUMBER: EP 04105484.2
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                                                                                                                                                                                                                                                                            LENGTH: 1000
                                                                                                                                                                 Local Similarity
185
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CTTCTTTGTAAATTAGCTCTTT 164
                               crrccrrcragaraacrrcrer 711
                                                                     CTGCATCTGAAGGCTGATCTTTACAACACCATTCTTGCTTCTTCTTCCCAATCCATGA 186
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Mulligan, Karl
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Pred. No. 0.011;
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US-11-266-748A-475045

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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
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; ORGANISM: Homo Sapiens
US-11-266-748A-475045
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Willigan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55915-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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    APPLICATION 1
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: 2004-11-03
NUMBER: EP 04105507.0
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Pred. No. 0.028;
"Midmatches 21;
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105482.6
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105507.0
PRIOR APPLICATION NUMBER: ED 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                               SEQ ID NO 105295
                                                                                                         Query Match
Best Local :
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LENGTH: 1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 483996
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NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
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                                                                                                                                                                                                                                          ENGTH:
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                                                                                  Local Similarity
nes 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 61; Conserv
                                         630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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690 CTTCCTTGTAGATAAGTTCTGT 711
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74.4%;
                                                                                  Score 48.4; DB Pred. No. 0.03; 0; Mismatches
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                                                                                                                          DB 8;
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371

CTTCTTTGTAAATTAGCTCTTT 350

690 CTTCCTTGTAGATAAGTTCTGT

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RESULT 19
US-11-266-748A-349487/c
US-11-266-748A-349487, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
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; ORGANISM: Homo Sapiens
US-11-266-748A-122015
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US-11-266-748A-122015
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Best Local Similarity
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                                                                  APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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                                              PRIOR APPLICATION NUMBER: EP 04105479.2
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105482.6
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FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
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APPLICATION NUMBER: EP 04105483.4
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; ORGANISM: Homo Sapiens
US-11-266-748A-432866
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US-11-266-748A-349487
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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                       Query Match
Best Local Similarity
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-03-14
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
                                                                                                                                                               ENGTH:
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Local Similarity 74.4%;
es 61; Conservative
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Mulligan, Karl
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                       6.0%;
Score 48.4; DB 8;
Pred. No. 0.035;
0; Mismatches 21;
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                                             Length 1928;
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Conservative

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; NAME/KEY: CDS
; LOCATION: (50)...(1324)
; OTHER INFORMATION: JNK2 variant 4
US-11-283-329-231
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; OTHER INFORMATION: JNK2 variant 1
US-11-283-329-225
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US-11-283-329-225/c
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GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 74.4
Matches 61; Conservative
                                                                                                                                             SOFTWARE: Fa
SEQ ID NO 231
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Sequence 231, Application US/11283329 Publication No. US20060134670A1
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                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
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CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
                                                                                                                                                        PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                       APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
                                                                                                                                                                                                                                                                          FILE REFERENCE: ACADIA.043A
                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
                                                                       FEATURE:
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74.4%;
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Pred. No. 0.035;
0; Mismatches
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RESULT 24
US-11-266-748A-242782
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US-11-266-748A-182241/c
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PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
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Best Local S
Matches 61
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn
SEQ ID NO 182241
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                                                                                                                        Sequence 242782, Application US/11266748A Publication No. US20060134663A1
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Best Local Similarity
Matches 61; Conserv
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NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0112 (319189) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: US 60/700,293
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Mulligan, Karl
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; ORGANISM: Homo Sapiens
US-11-266-748A-242782
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 227
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Publication No. US20060134670A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Piu, Fabrice
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                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1198)
OTHER INFORMATION: JNK2 variant 2
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FILING DATE: 2005-03-14
APPLICATION NUMBER: US 60/700,293
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                               .638 GAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTACTTCCTTG 697
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Similarity 74.4%;
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                                                                              Conservative
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77.0%;
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                                                                                               Score 46.8; DB 8; Pred. No. 0.085;
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                                                                          Mismatches
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626 GTACCTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTC 685

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US-11-283-329-217/c
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US-11-283-329-229/c
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Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 242
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 229
LENGTH: 1947
 Matches
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                Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                  LENGTH: 1412
TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
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TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
                                                                                NAME/KEY: CDS
LOCATION: (18)...(1301)
OTHER INFORMATION: JNK1 variant 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/629,811 PRIOR FILING DATE: 2004-11-19
                                                                                                                                         FEATURE:
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OTHER INFORMATION: JNK2 variant
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NAME/KEY: CDS
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77.0%;
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Score 44.4; DB Pred. No. 0.29; 0; Mismatches
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.085;
                                  DB 8;
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 26;
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                                  Length 1412;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
 Gaps
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; TYPE: DNA
; ORGANISM: OFFICE SETION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK099904
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-449-902-24462/c
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US-11-283-329-223/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 223
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24462, Application US/10449902
Publication No. US20060123505A1
                                                                                                                                        SEQ ID NO 24462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 223, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver 2.1
                                                                                                                                                                                                                                                                          APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ACADIA 043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS
TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (18)...(1301)
OTHER INFORMATION: JNK1 variant 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                   LENGTH: 1676
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o. US20060134670A1
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
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US-11-266-748A-395934/c
; Sequence 395934, Application US/11266748A
; Publication No. US20060134663A1
                                                                                                                                                                                                                             ; ORGANISM: Homo Sapiens
US-11-266-748A-395934
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                                                                                                                                                   Matches
                                                                                                                                                                                       Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EP 04105484.2 PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/700,293 FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/662,276 FILING DATE: 2005-03-14
                                                                         738
                                                                                               630 CTGAAGGAGAAGGCTGTCCTTTTACTACACCATTTTTTAGTCTTTTCTTCTGAATTCATTA 689
678 CTTCCTTATATATCAATTCTTT
                                   690 CTTCCTTGTAGATAAGTTCTGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 TCTGCTCTTTAAGCAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGA 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%;
l Similarity 69.5%;
57; Conservation
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                                                                                                                                                                                                                                                                                       1000
                                                                         CTAAAGGAGGGCTGCCCCGTATAACTCCATTCTTGGTTCTCTCCTCCAAGTCCATAA
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Mulligan, Karl
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Pred. No. 0.6;
0; Mismatches
                                                                                                                                                                     Score 42; E
Pred. No. 1;
657
                                                                                                                                                   Mismatches
                                                                                                                                                                                       DB 8; Length 1000,
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                                                                                                                                               25,
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                                                                                                                                                   Indels
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RESULT 31 US-11-266-748A-466980

Sequence 466980, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:

Johnston, Patrick Mulligan, Karl

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; ORGANISM: Homo Sapiens
US-11-266-748A-466980
                                                                                    US-11-283-329-219
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 219, Applic Publication No. US20 GENERAL INFORMATION:
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LENGTH: 1000
                                        Query Match
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                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS FILE REFERENCE: ACADIA, 043A CURRENT APPLICATION NUMBER: US/11/283,329 CURRENT FILING DATE: 2005-11-18 PRIOR APPLICATION NUMBER: 60/629,811 PRIOR FILING DATE: 2004-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
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CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Piu,
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                                                                                                        NAME/KEY: CDS
LOCATION: (18)...(1172)
OTHER INFORMATION: JNK1 variant 2
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                        LENGTH: 1417
                  Match 5.2%;
Local Similarity 69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/700,293 FILING DATE: 2005-07-18
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APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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APPLICATION NUMBER: EP 04105507.0
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APPLICATION NUMBER: EP 04105484.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          630 CTGAAGGAGAAGGCTGTCCTTTACTACACCATTTTTAGTCTTTTCTTCTGAATTCATTA 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/11283329 o. US20060134670A1
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Score 42; DB 8; Length 1417; Pred. No. 1.1; 0; Mismatches 25; Indels
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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  0
  Gaps
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILTR REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILLING DATE: 2004-11-03
PRIOR PILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILLING DATE: 2004-11-03
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; ORGANISM: Homo sapiens
; PRATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1172)
; OTHER INFORMATION: JNK1 variant 3
US-11-283-329-221
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; Sequence 349577, Application US/11266748A
; Publication No. US20060134663A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 1417
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APPLICANT: Piu, Fabrice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
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CURRENT FILING DATE: 2005-11-18
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APPLICANT: Johnston, F
APPLICANT: Mulligan, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1155 CTAAAGGAGAGGGCTGCCCCGTATAACTCCATTCTTGGTTCTCTCCTCCAAGTCCATAA 1096
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Mulligan, Karl
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PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105482.6
PRIOR PPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PRIOR PRIOR DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
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US-11-266-748A-349577
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LENGTH: 1943
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 349577
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Publication No. US20060134663A1
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Best Local :
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ORGANISM: Homo Sapiens
-11-266-748A-382413
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NUMBER OF SEQ ID NOS: 483996
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FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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876 CTTCCTTATATATCAATTCTTT 855
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Similarity 69.5%;
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Similarity 69.5%;
                                       CTTCCTTGTAGATAAGTTCTGT 711
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Pred. No. 1.2;
0; Mismatches 2
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105482.6
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105483.4
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
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US-11-266-748A-432956
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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Matches
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Publication No. US20060134663A1
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SEQ ID NO 432956
LENGTH: 1943
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57; Conserv
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; ORGANISM: Homo Sapiens
US-11-266-748A-24382
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SEQ ID NO 1069
LENGTH: 807
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 24382
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Best Local Similarity
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ORGANISM: Glycine max
-11-216-545-1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
TITLE OF INVENTION: Soybeans.
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
PRIOR FILING DATE: 2004-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MONSANTO Technology, LLC APPLICANT: McLaird, Paul L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIOR APPLICATION NUMBER: EP 04105485.9
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774
                                  476 AAGAAATAAAACTAAAATCATTATAAGGACACAA 509
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                                                                                                      594 AAATTAGACTGATATTAATATTCCCTCCGTCCCTGCCTATTTATAAGACATGTTTTTT 653
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                                                                                                                                                                                                                                                296 ACATTGACTTGATGGTCAAAAGGGCATTATGGCTCTGAATTTTGATGAGGCACATTTACC
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49.5%;
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Pred. No. 1.5;
0; Mismatches 108;
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Pred. No. 1.5;
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NAME/KEY: misc feature
; LOCATION: (564) . (564)
; OTHER INFORMATION: n is
US-11-266-748A-207992
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US-11-266-748A-207992/c
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                                                                                                                                                                                                                                                                                                                           Matches 107;
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
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NUMBER OF SEQ ID NOS: 483996
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NAME/KEY: misc_feature
LOCATION: (544)..(544)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (462)..(462)
OTHER INFORMATION: n is
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ORGANISM: Homo Sapiens
                                                                                                                     491
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165
                                      551
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                                                                                                                   AATCATTATAAGGACACAACCATGTGATATTTGTCCATCTGCTCTTTAAGCAATGTTATG
TTTATTGGTACATCACAATAAGATAGTGTTAAATATT 129
                                    TTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATT 587
                                                                             ATTTGTTCATGCTTTAATTTTTTCTGATTTGTTTCAATGTGGGTTTTTTGTTTTGTTTTG
                                                                                                                                                            CATTGTTATAATTAGAGCCTTAAGTTGTGGGACTTTTATTCTTATTATATACTATATAAA
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Pred. No. 1.5;
0; Mismatches 110;
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RESULT 40 US-10-539-228-134/c

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US-11-222-810-10
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Best Local S
Matches 90
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Publication No.
                                                                                                                                                                        Query Match
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APPLICANT: MUNNICH, Arnold
TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
FILE REFERENCE: 2121-0140P
CURRENT APPLICATION NUMBER: US/11/222,810
CURRENT FILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: US/99/109,082
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Publication N
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PRIOR APPLICATION NUMBER: 08/545,196
PRIOR FILING DATE: 1995-10-19
NUMBER OF SEQ ID NOS: 65
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NAME/KEY: misc feature

LOCATION: (1)...(139326)

OTHER INFORMATION: n = A,T,C or

-10-539-228-134
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CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 866
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.2
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APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: CHIR0052-101 (PP023370.0003)
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                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                Local Similarity 54.8
nes: 80; Conservative
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                                                       1423 CATTGTACTGTTTTTTTCTATCTTCTATATGTTTAAAAGTATATAAAAAAATATTTAAT
424 CCTGGATCATTACCATCAGAATAATCAGAATGAATGCCACACTGAATATCAAAAGAAATA 483
                                                                                          356 СТТТАССССАТСТТААСАТТТТСТТСАССАТТСАТТАСТАТТААЛАТТАТТАТСАЛАЛА 415
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54.8%;
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                                                                                                                                Score 40.4; DB Pred. No. 2.8; 0; Mismatches
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Pred. No. 9;
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105483.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105485.9
PRIOR APPLICATION NUMBER: ED 04105484.2
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US-11-222-810-12
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APPLICANT: Johnsto
APPLICANT: Mulliga
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APPLICANT: MUNNICH, Arnold
TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
FILE REFERENCE: 2121-0140P
CURRENT APPLICATION NUMBER: US/11/222,810
CURRENT FILING DATE: 2005-09-12
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SOFTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 08/545,196
PRIOR FILING DATE: 1995-10-19
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/662,276
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Mulligan, Karl
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Pred. No. 2.8;
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
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; ORGANISM: Homo Sapiens
US-11-266-748A-41216
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Best Local S
Matches 63
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SEQ ID NO 41216
LENGTH: 557
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                                                                                                                                                             Matches 63;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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APPLICATION NUMBER: US 60/700,293
FILING DATE: 2005-07-18
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
168
                                    756 CACAGGGAAATTCATTACTTAATGCCAAATAATTACGTTTTG 797
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                                                                            CACAATTAAGTACAATTATTTATGGAGAAAATTTTTACTATG 132
                                                                                                                                                             Conservative
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Pred. No. 3
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Pred. No. 3.2;
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 148014
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paurick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (3)9189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.7
PRIOR APPLICATION NUMBER: EP 04105487.0
PRIOR APPLICATION NUMBER: EP 04105487.0
PRIOR APPLICATION NUMBER: EP 04105487.0
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; Sequence 117427, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-148014
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US-11-266-748A-148014
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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APPLICANT: Johnston, I
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Mulligan, Karl
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FILING DATE:

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; ORGANISM: Homo Sapiens
US-11-266-748A-117427
                                                                                                                                                                                                               SOFTWARE: Patentin
SEQ ID NO 159591
                                                                        Matches
                                                                                          Best Local
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                                                                                                                                            ORGANISM: Homo Sapiens
-11-266-748A-159591
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT PRICTON UNMERR: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                              TYPE: DNA
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les 63; Conservative
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APPLICATION NUMBER: EP 04105484.2
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                                                                                          Similarity
TGTAGATAAGTTCTGTAAGAAACAGCTGTGTTATTATAGAAAACAAATTTATCCTTCATC 755
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Pred. No. 3
                                                                      Mismatches
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US-11-266-748A-222651
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; Sequence 222651, Application US/11266748A
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Best Local :
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                                                            APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
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                       APPLICATION NUMBER: EP 04105482.6 FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105483.4
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FILING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105507.0

2004-11-03

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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-340622
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; ORGANISM: Homo Sapiens
US-11-266-748A-289193
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LENGTH: 1000
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Best Local Similarity 61.8
Matches 63; Conservative
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SEQ ID NO 289193
                                             Query Match
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APPLICANT: Mulligan, Karl
ITTLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same.
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
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PRIOR FILING DATE: 2004-11-03
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
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Local Similarity 61.8%; Pred. No. 3.9;
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APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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APPLICATION NUMBER: EP 04105507.0
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APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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APPLICATION NUMBER: EP 04105484.2
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Pred. No. 3.9;
0; Mismatches
                                               DB 8; Length 1000;
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